

Db 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTGVSSVHNLHIKQLYH 300
Qy 301 SDEFRAYDGNADNKKHYNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Db 301 SDEFRAYDGNADNKKHYNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Qy 361 SLVLVSLLEPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 SLVLVSLLEPEWPTDFVWGLDAPQRMFSGNHL 395

RESULT 2
US-10-056-744B-2
; Sequence 2, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; FILE REFERENCE: HYDROLASE AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/10/056,744B
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-2

Query Match 95.08; Score 2030; DB 9; Length 398;
Best Local Similarity 97.28; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

Qy 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 60
Db 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 60
Qy 61 LVNRIPIYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWGMNSR 120
Db 61 LVNRIPIYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWGMNSR 120
Qy 121 GNTWSRRHKTLSSETDEKFWAFSDPMAYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
Db 121 GNTWSRRHKTLSSETDEKFWAFSDPMAYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
Qy 181 VAFSTMPPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTK 240
Db 181 VAFSTMPPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTK 240
Qy 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTGVSSVHNLHIKQLYH 300
Db 241 IASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTGVSSVHNLHIKQLYH 300
Qy 301 SDEFRAYDGNADNKKHYNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Db 301 SDEFRAYDGNADNKKHYNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 360
Qy 361 SLVLVSLLEPEWPTDFVWGLDAPQRMFSGNHL 390
Db 361 SLH-YFKLLPDNN-HDFVWGLDAPQRMYS 388

RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-4

Query Match 51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

Qy 2 MWLLLTTCICGTLNAGGFLDLENEVPEVMNTSEIIYNGYPSEYEVTTEDGYIL 61
Db 1 MRFLGLVCLVLTLSHSGGKLTAVDPETNNVSEIIISYMGFPSEYLVETEDGYIL 60
Qy 62 VNRIPYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWGMNSR 121
Db 61 LNRIPYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWGMNSR 120
Qy 122 NTSRRHKTLSSETDEKFWAFSDPMAYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 181
Db 121 NTSRRHKTLSSETDEKFWAFSDPMAYDLPVGTDFVNTKGTQEKLYFIGHSLGTTIGF 180
Qy 182 AFSTMPPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTK 241
Db 181 AFSTMPPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTK 240
Qy 242 ASTKICNNKILWLCSEFMSLWAGSKNNQSRMDVYMSHAPTGVSSVHNLHIKQLYH 301
Db 241 LGTHVCTHVLKELCGNLCLFCGNERNLNMSRVDVITTHSPAGTSVQNMHLWSQAKF 300
Qy 302 DEFRAYDGNADNKKHYNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTPQDVARIILPQIK 361
Db 301 QKQAFDNGSAAKYNFYNSYPTTYNVKMDLVPTAVWSGGHDLADYDVNILLTQITN 360
Qy 362 LSLVLVSLLEPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFHEH-IPWE-HLDFWGLDAPWRLYKINL 392

RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE REFERENCE: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-41

Query Match 51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;

XX PS Claim 1: Fig 2; 68pp; English.

XX CC The present invention provides the protein, coding and genomic sequences

XX CC of a human lysosomal acid lipase. The sequences can be used in the

XX CC identification of modulators of lipase activity in cells and tissues that

XX CC express the lipase, particularly the severe infantile-onset Wolman

XX CC disease and the milder late-onset cholesteryl ester storage disease

XX CC (CESD), which are caused by mutations in different parts of the lysosomal

XX CC acid lipase (LIPA) gene. The present sequence is the protein of the

XX CC invention.

XX SQ Sequence 395 AA;

Query Match 100.0%; Score 2137; DB 23; Length 395;

Best Local Similarity 100.0%; Pred. No. 3.4e-206;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVWMTSEIIYNGYSPSEEVETEDGYIL 60

DB 1 MWLLLTTCICGTLNAGGFLDLENEVPEVWMTSEIIYNGYSPSEEVETEDGYIL 60

QY 61 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120

DB 61 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120

QY 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180

DB 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180

QY 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

DB 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

QY 241 IASTKICNNKILWILICSEFMSLWAGSNKKNNQSRMDVYVSHAPTGSVHNILHIKOLYH 300

DB 241 IASTKICNNKILWILICSEFMSLWAGSNKKNNQSRMDVYVSHAPTGSVHNILHIKOLYH 300

QY 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKYPTAIWAGGHDVLGTPODVARILPOIK 360

DB 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKYPTAIWAGGHDVLGTPODVARILPOIK 360

QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395

DB 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395

RESULT 2

AAU98539

ID AAU98539 standard; Protein; 427 AA.

XX AC AAU98539;

XX DT 21-AUG-2002 (first entry)

XX DE Human lysosomal acid lipase protein #2.

XX KW Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;

XX KW central nervous system disorder; chronic obstructive pulmonary disease;

XX KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;

XX KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;

XX KW congestive heart failure; myocardial infarction.

XX OS Homo sapiens.

XX PN WO200236754-A2.

XX PD 10-MAY-2002.

XX XX 26-OCT-2001; 2001WO-EP12382.

XX PF 31-OCT-2000; 2000US-244215P.

XX PR 06-DEC-2000; 2000US-251401P.

XX (FARB) BAYER AG.

XX xiao Y;

XX WPI: 2002-490007/52.

XX N-PSDB; ABK85978.

XX Novel human lysosomal acid lipase polypeptide, useful for treating

XX cancer, central nervous system disorder, obesity, chronic obstructive

XX pulmonary disease, diabetes or cardiovascular disorder

XX Claim 1: Fig 5; 126pp; English.

XX This invention relates to the DNA and protein sequences of a purified

XX human lysosomal acid lipase protein. The sequences of the invention are

XX useful for screening for agents which modulate the activity of human

XX lysosomal acid lipase polypeptide. A compound which increases human

XX lysosomal acid lipase activity may be identified as a potential

XX therapeutic agent for increasing the activity of the human lysosomal

XX acid lipase, and a test compound which decreases the human lysosomal

XX acid lipase activity is identified as a potential therapeutic agent for

XX decreasing the activity of human lysosomal acid lipase. A pharmaceutical

XX compound containing the lysosomal acid lipase sequences is useful for

XX the preparation of a medicament for modulating the activity of human

XX lysosomal acid lipase in a disease such as cancer, central nervous

XX system (CNS) disorder, obesity, chronic obstructive pulmonary disease,

XX diabetes or a cardiovascular disorder. A reagent that modifies the

XX activity of the protein of the invention is useful for treating a human

XX lysosomal acid lipase dysfunction related disease, preferably the above

XX mentioned diseases. A DNA or protein sequence of the invention is

XX useful for treating the above mentioned disorders, where the CNS

XX disorders are selected from Alzheimer's and Parkinson's disease,

XX dementia, multiple sclerosis, Huntington's disease, and pain, and the

XX cardiovascular disorder is selected from congestive heart failure and

XX myocardial infarction. The present sequence represents a human lysosomal

XX acid lipase protein of the invention, the gene encoding this protein is

XX located on human chromosome 10.

XX SQ Sequence 427 AA;

Query Match 95.0%; Score 2030; DB 23; Length 427;

Best Local Similarity 97.2%; Pred. No. 2.2e-195;

Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVWMTSEIIYNGYSPSEEVETEDGYIL 60

DB 30 MWLLLTTCICGTLNAGGFLDLENEVPEVWMTSEIIYNGYSPSEEVETEDGYIL 89

QY 61 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 120

DB 90 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDWMGNSR 149

QY 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 180

DB 150 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPGVDFIVNKTGOEKLIFGHSLGTTIGF 209

QY 181 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

DB 210 VAFSTPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 269

QY 241 IASTKICNNKILWILICSEFMSLWAGSNKKNNQSRMDVYVSHAPTGSVHNILHIKOLYH 300

DB 270 IASTKICNNKILWILICSEFMSLWAGSNKKNNQSRMDVYVSHAPTGSVHNILHIKOLYH 329

QY 301 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKYPTAIWAGGHDVLGTPODVARILPOIK 360

DB 330 SDEFRAYDNGNDADNMKHYNQSHPPYIDLTAMKYPTAIWAGGHDVLGTPODVARILPOIK 389

QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFS 390

DB 390 SLH-YFKLLPDWN-HFDVWGLDAPQRMYS 417

Thu Apr 3 09:00:15 2003

Db 241 IASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 300
QY 301 SDEFAYDNGNDADNNKHYNQSHPPYDITAMKVPYTAIWAGGHDVLTGTPQDVARIILPQIK 360
Db 301 SDEFAYDNGNDADNNKHYNQSHPPYDITAMKVPYTAIWAGGHDVLTGTPQDVARIILPQIK 360
QY 361 SLSVLSSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 SLSVLSSLPEWPTDFVWGLDAPQRMFSGNHL 395

RESULT 2
US-10-056-744B-2
; Sequence 2, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; FILE REFERENCE: HYDROLASE AND USES THEREFOR
; CURRENT FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-2

Query Match 95.0%; Score 2030; DB 9; Length 398;
Best Local Similarity 97.2%; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSSEYEVTTEDGYIL 60
Db 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSSEYEVTTEDGYIL 60
QY 61 LVNRPYGRTHARSTGPRPVYMQHALFADNAYWLENANGSLGFLLDAGYDVWNGNSR 120
Db 61 LVNRPYGRTHARSTGPRPVYMQHALFADNAYWLENANGSLGFLLDAGYDVWNGNSR 120
QY 121 GNTWRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 180
Db 121 GNTWRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 180
QY 181 VAFSTMPELAQRKMNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
Db 181 VAFSTMPELAQRKMNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 241 IASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 300
Db 241 IASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 300
QY 301 SDEFAYDNGNDADNNKHYNQSHPPYDITAMKVPYTAIWAGGHDVLTGTPQDVARIILPQIK 360
Db 301 SDEFAYDNGNDADNNKHYNQSHPPYDITAMKVPYTAIWAGGHDVLTGTPQDVARIILPQIK 360
QY 361 SLSVLSSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 SLH-YFKLLPDWN-HDFVWGLDAPQRMYS 388

RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-4

Query Match 51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;
QY 2 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSSEYEVTTEDGYIL 61
Db 1 MRFLGLVCLVLTWTLHSEGGKLTAVDPETNMNVSEIIYWGPPSEYEVTTEDGYIL 60
QY 62 VNRIYGRTHARSTGPRPVYMQHALFADNAYWLENANGSLGFLLDAGYDVWNGNSR 121
Db 61 LNRIPGKRNHSDKPKPVVFLQHLGLDSSNWTNLSNLSGLFLLADAGYDVWNGNSR 120
QY 122 NTSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 181
Db 121 NTSRRHKTLSSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTIGF 180
QY 182 AFSTMPELAQRKMNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 241
Db 181 AFSTMPELAQRKMNALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYH 301
Db 241 LGTHVCHTHVILKELCGNLCFLCGFNERNLNMSRDVYTHSPAGTSVQNMHLWSQAVKE 300
QY 302 DEFAYDNGNDADNNKHYNQSHPPYDITAMKVPYTAIWAGGHDVLTGTPQDVARIILPQIK 361
Db 301 QKQAFDNGSNAKVFHYNQSYPTYNVKMLVPTAVWNGHDLADYDVWNLITQITN 360
QY 362 LSLVSSLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFHES-IPWE-HLDFIWGLDAPWRLYNNKIINL 392

RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-6U2
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-41

Query Match 51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;

XX PS Claim 1; Fig 2; 68pp; English.

XX CC The present invention provides the protein, coding and genomic sequences

CC of a human lysosomal acid lipase. The sequences can be used in the

CC identification of modulators of lipase activity in cells and tissues that

CC express the lipase, particularly the severe infantile-onset Wolman

CC disease and the milder late-onset cholesteryl ester storage disease

CC (CESD), which are caused by mutations in different parts of the lysosomal

CC acid lipase (LIPA) gene. The present sequence is the protein of the

CC invention.

XX Sequence 395 AA;

XX Query Match 100.0%; Score 2137; DB 23; Length 395;

XX Best Local Similarity 100.0%; Pred. No. 3.4e-206;

XX Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLLTTCICGTLNAGGFLDENEVPEVWMTSEIIYNGYSEEVETEDGYIL 60

Db 1 MWLLLTTCICGTLNAGGFLDENEVPEVWMTSEIIYNGYSEEVETEDGYIL 60

QY 61 LVNRIPIGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

Db 61 LVNRIPIGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFTGHSLGTTIGF 180

Db 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFTGHSLGTTIGF 180

QY 181 VAFSTPELAQRKMNFPALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

Db 181 VAFSTPELAQRKMNFPALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

QY 241 IASTKICNNKILWLCSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

Db 241 IASTKICNNKILWLCSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

QY 301 SDEFRAYDNGNDADNMKNHYNOSHPPIYDLTAMKVPTAIWAGGHVDVLTGTPQDVARILPOIK 360

Db 301 SDEFRAYDNGNDADNMKNHYNOSHPPIYDLTAMKVPTAIWAGGHVDVLTGTPQDVARILPOIK 360

QY 361 SLSLVSLLEPEWPTDFVWGLDAPQRMFSGNHNL 395

Db 361 SLSLVSLLEPEWPTDFVWGLDAPQRMFSGNHNL 395

RESULT 2

AAU98539

ID AAU98539 standard; Protein; 427 AA.

.XX AC AAU98539;

XX 21-AUG-2002 (first entry)

XX Human lysosomal acid lipase protein #2.

XX Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;

XX central nervous system disorder; chronic obstructive pulmonary disease;

XX diabetes; cardiovascular disorder; Alzheimer's disease; dementia;

XX Parkinson's disease; multiple sclerosis; Huntington's disease; pain;

XX congestive heart failure; myocardial infarction.

XX Homo sapiens.

XX OS

XX WO200236754-A2.

XX PN

XX 10-MAY-2002.

XX PD

XX 26-OCT-2001; 2001WO-EPI2382.

XX PF

XX 31-OCT-2000; 2000US-244215P.

XX PR

XX 06-DEC-2000; 2000US-251401P.

XX PA (FARB) BAYER AG.

XX PI xiao Y;

XX WPI: 2002-490007/52.

DR N-PSDB; ABK85978.

XX Novel human lysosomal acid lipase polypeptide, useful for treating

PT cancer, central nervous system disorder, obesity, chronic obstructive

PT pulmonary disease, diabetes or cardiovascular disorder

XX Claim 1; Fig 5; 126pp; English.

PS This invention relates to the DNA and protein sequences of a purified

XX human lysosomal acid lipase protein. The sequences of the invention are

CC useful for screening for agents which modulate the activity of human

CC lysosomal acid lipase polypeptide. A compound which increases human

CC lysosomal acid lipase activity may be identified as a potential

CC therapeutic agent for increasing the activity of the human lysosomal

CC acid lipase, and a test compound which decreases the human lysosomal

CC acid lipase activity is identified as a potential therapeutic agent for

CC decreasing the activity of human lysosomal acid lipase. A pharmaceutical

CC compound containing the lysosomal acid lipase sequences is useful for

CC the preparation of a medicament for modulating the activity of human

CC lysosomal acid lipase in a disease such as cancer, central nervous

CC system (CNS) disorder, obesity, chronic obstructive pulmonary disease,

CC diabetes or a cardiovascular disorder. A reagent that modifies the

CC activity of the protein of the invention is useful for treating a human

CC lysosomal acid lipase dysfunction related disease, preferably the above

CC mentioned diseases. A DNA or protein sequence of the invention is

CC useful for treating the above mentioned disorders, where the CNS

CC disorders are selected from Alzheimer's and Parkinson's disease,

CC dementia, multiple sclerosis, Huntington's disease, and pain, and the

CC cardiovascular disorder is selected from congestive heart failure and

CC myocardial infarction. The present sequence represents a human lysosomal

CC acid lipase protein of the invention, the gene encoding this protein is

CC located on human chromosome 10.

XX Sequence 427 AA;

XX Query Match 95.0%; Score 2030; DB 23; Length 427;

XX Best Local Similarity 97.2%; Pred. No. 2.2e-195;

XX Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 1 MWLLLTTCICGTLNAGGFLDENEVPEVWMTSEIIYNGYSEEVETEDGYIL 60

Db 30 MWLLLTTCICGTLNAGGFLDENEVPEVWMTSEIIYNGYSEEVETEDGYIL 89

QY 61 LVNRIPIGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120

Db 90 LVNRIPIGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 149

QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFTGHSLGTTIGF 180

Db 150 GNTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYFTGHSLGTTIGF 209

QY 181 VAFSTPELAQRKMNFPALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 240

Db 210 VAFSTPELAQRKMNFPALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTK 269

QY 241 IASTKICNNKILWLCSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 300

Db 270 IASTKICNNKILWLCSEFMSLWAGSNKKNQSRMDVYMSHAPTGSVHNILHIKOLYH 329

QY 301 SDEFRAYDNGNDADNMKNHYNOSHPPIYDLTAMKVPTAIWAGGHVDVLTGTPQDVARILPOIK 360

Db 330 SDEFRAYDNGNDADNMKNHYNOSHPPIYDLTAMKVPTAIWAGGHVDVLTGTPQDVARILPOIK 389

QY 361 SLSLVSLLEPEWPTDFVWGLDAPQRMFS 390

Db 390 SLH-YFKLLPDWN-HFEVWGLDAPQRMYS 417

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:35:22 ; Search time 77 seconds
(without alignments)
683.558 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLTTTCLICLTNAGG.....FDFWGLDAPQMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2137	100.0	395	AAO18226	Human lysosomal ac
2	2030	95.0	427	AAU98539	Human lysosomal ac
3	2009	94.0	403	AAU77493	Human lipid metabo
4	1823	85.3	365	AAE17307	Human lysosomal ac
5	1242	58.1	397	AAE17308	Human lysosomal ac
6	1108	51.8	311	AAU98540	Human lysosomal ac
7	1097	51.3	392	AAO18227	Human lysosomal ac
8	1091	51.1	399	AAU980783	Human shear stress
9	1091	51.1	399	AAU980783	Human lysosomal ac
10	1052	49.2	398	7 AAP60724	Sequence of pregas

11	1052	49.2	398	7 AAP60658	Sequence of human
12	1052	49.2	398	17 AAU09383	Human gastric lipa
13	1052	49.2	398	22 AAB66086	Human lipase prote
14	1031	48.2	409	22 AAE11931	Human CGI62 (or C5
15	1031	48.2	423	22 AAB66065	Human TANGO 294.
16	1030	48.2	395	23 AAE14744	Human triacylglyce
17	1030	48.2	399	23 AAU77496	Human lipid metabo
18	1027	48.1	398	14 AAU37302	RGL precursor. Or
19	1026	48.0	399	22 AAG67513	Amino acid sequenc
20	1023	47.9	390	22 AAB66067	Human TANGO 294 ma
21	1014.5	47.5	395	6 AAP50322	Rat lingual lipase
22	1004	47.0	379	15 AAR56870	Canine gastric lip
23	1004	47.0	379	17 AAU09382	Dog gastric lipase
24	1004	47.0	380	15 AAR56871	Canine gastric lip
25	995	46.6	398	23 AAU99164	Human lysosomal ac
26	989.5	46.3	449	22 AAU30498	Novel human secret
27	972	45.5	378	23 ABB76189	Kid goat pregastr
28	913.5	42.7	371	23 AAU99165	Human lysosomal ac
29	798	37.3	731	23 AAE14746	Human triacylglyce
30	723	33.8	276	23 AAE14745	Human triacylglyce
31	723	33.8	289	23 AAU77494	Human lipid metabo
32	700	32.8	221	22 AAB66068	Human TANGO 294 ex
33	672.5	31.5	280	23 AAE14743	Human triacylglyce
34	661.5	31.0	656	22 ABB66839	Novel human diagno
35	643	30.1	233	22 AAB61608	Human protein HP03
36	561.5	26.3	399	22 ABB71442	Drosophila melanog
37	548.5	25.7	434	22 ABB62081	Drosophila melanog
38	546	25.5	456	22 ABB68957	Drosophila melanog
39	542.5	25.4	398	22 ABB63011	Drosophila melanog
40	533	24.9	394	22 ABB71702	Drosophila melanog
41	511.5	23.9	416	22 ABB59328	Drosophila melanog
42	508	23.8	457	22 ABB63187	Drosophila melanog
43	496.5	23.2	410	21 AAU32309	Soybean acid triac
44	495	23.2	435	22 ABB71506	Drosophila melanog
45	492.5	23.0	410	21 AAU32307	Rice acid triacylg

ALIGNMENTS

RESULT 1

AAO18226
ID AAO18226 standard; Protein; 395 AA.

XX AC AAO18226;

XX DT 18-SEP-2002 (first entry)

XX DE Human lysosomal acid lipase.

XX DE Human; lysosomal acid lipase; chromosome 10; lipemic; Wolman disease; cholesteryl ester storage disease.

XX OS Homo sapiens.

XX PN USG387680-B1.

XX PD 14-MAY-2002.

XX PF 29-MAR-2001; 2001US-0820001.

XX PR 29-MAR-2001; 2001US-0820001.

XX PA (PEKE) PE CORP NY.

XX PI Merkulo GV, Ketchum KA, Di Francesco V, Beasley EM;

XX DR WPI; 2002-478445/51.

XX DR N-PSDB; AAL47480, AAL47481.

XX Isolated nucleic acids encoding a lysosomal acid lipase protein useful for the prevention, diagnosis and treatment of severe infantile-onset PT Wolman disease and late-onset cholesteryl ester storage disease

```

XX PS Claim 1; Fig 2; 68pp; English.
XX
CC "The present invention provides the protein, coding and genomic sequences
CC of a human lysosomal acid lipase. The sequences can be used in the
CC identification of modulators of lipase activity in cells and tissues that
CC express the lipase, particularly the severe infantile-onset Wolman
CC disease and the milder late-onset cholesteryl ester storage disease
CC (CESD), which are caused by mutations in different parts of the lysosomal
CC acid lipase (LIPA) gene. The present sequence is the protein of the
CC invention.
XX
XX Sequence 395 AA;
XX
Query Match 100.0%; Score 2137; DB 23; Length 395;
Best Local Similarity 100.0%; Pred. No. 3.4e-206;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTEDGYIL 60
DB 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTEDGYIL 60
QY 61 LVNRIPIGTRHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
DB 61 LVNRIPIGTRHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPGVIDFIVNKTGOEKLFIHSLGTTIGF 180
DB 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPGVIDFIVNKTGOEKLFIHSLGTTIGF 180
QY 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDKTK 240
DB 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDKTK 240
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSDVMYMSHAPTGSSVHNLIHLKQLYH 300
DB 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSDVMYMSHAPTGSSVHNLIHLKQLYH 300
QY 301 SDEFRAYDNGNDADNKKHYNQSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
DB 301 SDEFRAYDNGNDADNKKHYNQSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395
DB 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFSGNHNL 395
RESULT 2
AAU98539
ID AAU98539 standard; Protein; 427 AA.
XX
AC AAU98539;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human lysosomal acid lipase protein #2.
XX
KW Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;
KW central nervous system disorder; chronic obstructive pulmonary disease;
KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;
KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;
KW congestive heart failure; myocardial infarction.
OS Homo sapiens.
XX
PN WO200236754-A2.
XX
PD 10-MAY-2002.
XX
PF 26-OCT-2001; 2001WO-EP12382.
XX
PR 31-OCT-2000; 2000US-244215P.
PR 06-DEC-2000; 2000US-251401P.
```

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XX PA (FARB ) BAYER AG.
XX PI Xiao Y;
XX WPI: 2002-490007/52.
XX N-PSDB: ABK85978.
XX
PT Novel human lysosomal acid lipase polypeptide, useful for treating
PT cancer, central nervous system disorder, obesity, chronic obstructive
PT pulmonary disease, diabetes or cardiovascular disorder -
XX
XX Claim 1; Fig 5; 126pp; English.
XX
XX This invention relates to the DNA and protein sequences of a purified
XX human lysosomal acid lipase protein. The sequences of the invention are
XX useful for screening for agents which modulate the activity of human
XX lysosomal acid lipase polypeptide. A compound which increases human
XX lysosomal acid lipase activity may be identified as a potential
XX therapeutic agent for increasing the activity of the human lysosomal
XX acid lipase, and a test compound which decreases the human lysosomal
XX acid lipase activity is identified as a potential therapeutic agent for
XX decreasing the activity of human lysosomal acid lipase. A pharmaceutical
XX compound containing the lysosomal acid lipase sequences is useful for
XX the preparation of a medicament for modulating the activity of human
XX lysosomal acid lipase in a disease such as cancer, central nervous
XX system (CNS) disorder, obesity, chronic obstructive pulmonary disease,
XX diabetes or a cardiovascular disorder. A reagent that modifies the
XX activity of the protein of the invention is useful for treating a human
XX lysosomal acid lipase dysfunction related disease, preferably the above
XX mentioned diseases. A DNA or protein sequence of the invention is
XX useful for treating the above mentioned disorders, where the CNS
XX disorders are selected from Alzheimer's and Parkinson's disease,
XX dementia, multiple sclerosis, Huntington's disease, and pain, and the
XX cardiovascular disorder is selected from congestive heart failure and
XX myocardial infarction. The present sequence represents a human lysosomal
XX acid lipase protein of the invention, the gene encoding this protein is
XX located on human chromosome 10.
XX
XX Sequence 427 AA;
XX
Query Match 95.0%; Score 2030; DB 23; Length 427;
Best Local Similarity 97.2%; Pred. No. 2.2e-195;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;
QY 1 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTEDGYIL 60
DB 30 MWLLLTTCICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTEDGYIL 89
QY 61 LVNRIPIGTRHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 120
DB 90 LVNRIPIGTRHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSR 149
QY 121 GNTWSRRHKTSETDEKFWAFSDEMAYDLPGVIDFIVNKTGOEKLFIHSLGTTIGF 180
DB 150 GNTWSRRHKTSETDEKFWAFSDEMAYDLPGVIDFIVNKTGOEKLFIHSLGTTIGF 209
QY 181 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDKTK 240
DB 210 VAFSTMPPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDKTK 269
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSDVMYMSHAPTGSSVHNLIHLKQLYH 300
DB 270 IASTKICNNKILWLICSEFMSLWAGSNKKNMQSDVMYMSHAPTGSSVHNLIHLKQLYH 329
QY 301 SDEFRAYDNGNDADNKKHYNQSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 360
DB 330 SDEFRAYDNGNDADNKKHYNQSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVARILPQIK 389
QY 361 SLSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
DB 390 SLH-YFKLLPDWN-HFDFVWGLDAPQRMYS 417
```

RESULT 3

AAU77493
 ID AAU77493 standard; Protein; 403 AA.
 AC AAU77493;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human lipid metabolism enzyme, LMM-1.
 XX
 KW Human; lipid metabolism enzyme; LMM-1; immune system disorder;
 KW neurological disorder; developmental disorder; cancer; nootropic;
 KW cell proliferative disorder; immunomodulator; neuroprotective;
 KW cytoskeletal; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200216597-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US26365.
 XX
 PR 23-AUG-2000; 2000US-227429P.
 PR 08-SEP-2000; 2000US-231370P.
 PR 15-SEP-2000; 2000US-233212P.
 PR 29-SEP-2000; 2000US-236885P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Griffin JA, Patterson C, Gandhi AR, Lu Y, Yao MG, Baughn MR;
 PI Walia NK, Hafalia AJA, Ding L, Tribouley CM, Das D, Thornton M;
 PI Lal P;
 XX
 DR WPI: 2002-280936/32.
 DR N-PSDB; ABK12385.
 XX
 PT New lipid metabolism enzymes, useful for diagnosing, treating or
 PT preventing immune system disorders (e.g. Crohn's disease), neurological
 PT disorders (e.g. Parkinson's disease), or cell proliferative disorders
 PT (e.g. cancers).
 XX
 PS Claim 45; Page 108-109; 122pp; English.
 XX
 CC The present invention relates to the isolation of human lipid
 CC metabolism enzymes (LMM) designated LMM-1 to LMM-6, and the
 CC polynucleotide sequences encoding them. The LMM polypeptides,
 CC polynucleotides, agonists and antagonists are useful for diagnosing,
 CC treating or preventing disorders associated with aberrant expression
 CC of LMM, particularly immune system disorders (e.g. acquired
 CC immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia,
 CC asthma or Crohn's disease), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, dementia or Parkinson's disease), developmental
 CC disorders (e.g. Down's syndrome) or cell proliferative disorders
 CC (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma or sarcoma). The present sequence represents human LMM-1.
 XX
 SQ Sequence 403 AA;
 Query Match 94.08; Score 2009; DB 23; Length 403;
 Best Local Similarity 96.24; Pred. No. 2.66-193;
 Matches 375; Conservative 3; Mismatches 10; Indels 2; Gaps 2;
 1 MWLLLTTCICGTNLNAGGFLDLENEVPEVWMTSEIIYNGVPSSEYEVTTEDGVIL 60
 6 MWLLLTTCICGTNLNAGGFLDLENEVPEVWMTSEIIYNGVPSSEYEVTTEDGVIL 65
 61 LVNRIPIYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLLDAGYDVMGNSR 120
 66 LVNRIPIYGRTHARSTGPRPVVYMQHALFAGQAYWLENYANGSLGFLLDAGYDVMGNSR 125
 121 GNTWSRRHKTLSSETDEKFWAFSDEMAYDLPVGVDFIVNKTQGEKLYFIGHSLGTTIGF 180

Db 126 GNTWSRRHKTLSSETDEKFWAFSDEMAYDLPVGVDFIVNKTQGEKLYFIGHSLGTTIGF 185
 Qy 181 VAFSTMPLELAORIKMNFALGPTISFKYPTGTFTRFELLPNLSIKAVFGTKGFLEDDKTK 240
 Db 186 VAFSTMPLELAORIKMNFALGPTISFKYPTGTFTRFELLPNLSIKAVFGTKGFLEDDKTK 245
 Qy 241 IASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPTGVSSVHNILHKNQLYH 300
 Db 246 IASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPTGVSSVHNILHKNQLYH 305
 Qy 301 SDEPRAYDWGNDADNMKHYNQSHPPYDILTAMKVPTAIWAGHDVLGTPQDVARILPQIK 360
 Db 306 SDEPRAYDWGNDADNMKHYNQSHPPYDILTAMKVPTAIWAGHDVLGTPQDVARILPQIK 365
 Qy 361 SLSLVLSLLPEWPTDFVWGLDAPQRMFS 390
 Db 366 SLH-YFKLLPDWN-HFDFVWGLDAPQRMYS 393

RESULT 4

AAE17307
 ID AAE17307 standard; Protein; 365 AA.
 AC AAE17307;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human lysosomal acid lipase protein, sbg236015LIPASE #1.
 XX
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;
 KW noctropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; lysosomal acid lipase.
 XX
 OS Homo sapiens.
 XX
 PN WO200198342-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US19929.
 XX
 PR 22-JUN-2000; 2000US-213156P.
 PR 22-JUN-2000; 2000US-213161P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdoch PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX
 DR WPI: 2002-139783/18.
 DR N-PSDB; AAD27802.
 XX
 PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities
 XX
 PS Claim 1; Page 105; 138pp; English.
 XX
 CC The invention relates to secreted and membrane-associated polypeptides

CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesterol ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
 CC allergies, schizophrenia, sbg42445PROA-associated disorders,
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human lysosomal acid lipase.

XX Sequence 365 AA;

Query Match 85.3%; Score 1823; DB 23; Length 365;
 Best Local Similarity 88.9%; Pred No. 1.2e-174;
 Matches 346; Conservative 2; Mismatches 7; Indels 34; Gaps 3;

QY 2 MWLLTTTCLICGTLNAGFLDLENEVPVNMNTSEIIYNGYPSSEYVETTEDGYILL 61
 Db 1 MWLLTTTCLICGTLNAGFLDLENEVPVNMNTSEIIYNGYPSSEYVETTEDGYILL 60
 QY 62 VNRIPYGRTHARSTGRPVVYQWHLAFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
 Db 61 VNRIPYGRTHARST-----ADAGYDVWNGNSRG 88
 QY 122 NTWSRRHKTLSRDEKFAFSEDEMAKYDLPGVDFIVNKTQGEKLYFGHSIGTIGFV 181
 Db 89 NTWSRRHKTLSRDEKFAFSEDEMAKYDLPGVDFIVNKTQGEKLYFGHSIGTIGFV 148
 QY 182 AFSTWPELAQRKMFALGPTISFKYPTGIFTRFELLPNSIIKAVFGTKGFLEDKTKKI 241
 Db 149 AFSTWPELAQRKMFALGPTISFKYPTGIFTRFELLPNSIIKAVFGTKGFLEDKTKKI 208
 QY 242 ASTKICNNKILICSEFNLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 301
 Db 209 ASTKICNNKILICSEFNLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 268
 QY 302 DEFRAYDGNADNADNKKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPDVARILPQIKS 361
 Db 269 DEFRAYDGNADNADNKKHYNQSHPPYIDLTAMKVPTAIWAGGHVLTGTPDVARILPQIKS 328
 QY 362 LSLVLSLPEWEPTDFVWGLDAPQRMFS 390
 Db 329 LH-YFKLLPDWN-HFDVWGLDAPQRMYS 355

RESULT 5
 ID AAEI7308 standard: Protein; 397 AA.
 XX AAEI7308;
 AC AAEI7308;
 XX AAEI7308;
 DT 18-APR-2002 (first entry)
 XX

DE Human lysosomal acid lipase protein, sbg236015LIPASE #2.
 KW Human; therapy: wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neutropenic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnerable; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; lysosomal acid lipase.
 XX Homo sapiens.
 XX WO200198342-A1.
 PN 27-DEC-2001.
 XX 22-JUN-2001; 2001WO-US19929.
 PF 22-JUN-2000; 2000US-213156P.
 PR 22-JUN-2000; 2000US-213161P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX WPI; 2002-139783/18.
 DR N-P5DB; AAD27803.
 XX Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities
 XX Claim 1; Page 106; 138pp; English.
 XX The invention relates to secreted and membrane-associated polypeptides
 CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesterol ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC allergies, schizophrenia, sbg42445PROA-associated disorders,
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.

CC The present sequence is human lysosomal acid lipase protein.

XX Sequence 397 AA;

Query Match 58.1%; Score 1242; DB 23; Length 397;

Best Local Similarity 60.1%; Pred. No. 3.7e-116;

Matches 235; Conservative 49; Mismatches 101; Indels 6; Gaps 4;

Qy 2 MWLLITTC--LICGLNAGGFLDLENVPEVMMNTSEIIYNGYPSSEYEVTTEDGYI 59

Db 1 MWQLLAACWMLLGSMT--GYDKGNANPEANNISQIISYWGYPSEYEDVTTKDYI 58

Qy 60 LLVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGLADAGYVMMGNS 119

Db 59 LGIYRPHGRGCPGRTAPKPAVYLQHGGLIASASNNICLPNNSLAFLADSGYDWLGN 118

Qy 120 RGNWRRHKTLSSETDEKFWAFSDEMAYDLPGVIDFVKNVGOEKLYFGHSLGTTIG 179

Db 119 RGNWRRHKTLSSETDEKFWAFSDEMAYDLPATINFIIEKTKGRLYYVGHSGQTTIA 178

Qy 180 FVASTMPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDEKKT 239

Db 179 FIAFTNPPELAKKIKIFALAPVVTYQSPMKLTTLSSRVKVLGDKMFPHTLFD 238

Qy 240 KIATKICNNKILWICSEFSLWAGSNKKNMOSRMDVYMSHAPTGGSVNHLIKOLY 299

Db 239 QFIATKVCNRKLFRRICSNFLTSLSGFDPQNLNRLDVYLSHNPAGTSVQNMHLHWAQY 298

Qy 300 HSDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHDVLTGTPQDVARILPQI 359

Db 299 HSDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHDVLTGTPQDVARILPQI 358

Qy 360 KSLSLVLLPEWEPTFDVFWGLDAPQRMFS 390

Db 359 KSLH-YFKLLPDWN-HFDVFWGLDAPQRMYS 387

RESULT 6

AAU98540

ID AAU98540 standard; Protein; 311 AA.

XX AAU98540;

XX AAU98540;

DT 21-AUG-2002 (first entry)

DE Human lysosomal acid lipase protein #3.

XX Human; lysosomal acid lipase; cancer; CNS; obesity; chromosome 10;
 KW central nervous system disorder; chronic obstructive pulmonary disease;
 KW diabetes; cardiovascular disorder; Alzheimer's disease; dementia;
 KW Parkinson's disease; multiple sclerosis; Huntington's disease; pain;
 KW congestive heart failure; myocardial infarction.

XX Homo sapiens.

OS WO200236754-A2.

FN 10-MAY-2002.

XX 26-OCT-2001; 2001WO-EPI2382.

XX 31-OCT-2000; 2000US-244215P.

PR 06-DEC-2000; 2000US-251401P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI; 2002-490007/52.

DR N-PSDB; ABK85969.

XX Novel human lysosomal acid lipase polypeptide, useful for treating
 PT cancer, central nervous system disorder, obesity, chronic obstructive
 DE

PT pulmonary disease, diabetes or cardiovascular disorder

XX Claim 1; Fig 6; 126pp; English.

XX This invention relates to the DNA and protein sequences of a purified
 CC human lysosomal acid lipase protein. The sequences of the invention are
 CC useful for screening for agents which modulate the activity of human
 CC lysosomal acid lipase polypeptide. A compound which increases human
 CC lysosomal acid lipase activity may be identified as a potential
 CC therapeutic agent for increasing the activity of the human lysosomal
 CC acid lipase, and a test compound which decreases the activity of the
 CC acid lipase activity is identified as a potential therapeutic agent for
 CC decreasing the activity of human lysosomal acid lipase. A pharmaceutical
 CC compound containing the lysosomal acid lipase sequences is useful for
 CC the preparation of a medicament for modulating the activity of human
 CC lysosomal acid lipase in a disease such as cancer, central nervous
 CC system (CNS) disorder, obesity, chronic obstructive pulmonary disease,
 CC diabetes or a cardiovascular disorder. A reagent that modifies the
 CC activity of the protein of the invention is useful for treating a human
 CC lysosomal acid lipase dysfunction related disease, preferably the above
 CC mentioned diseases. A DNA or protein sequence of the invention is
 CC useful for treating the above mentioned disorders, where the CNS
 CC disorders are selected from Alzheimer's and Parkinson's disease,
 CC dementia, multiple sclerosis, Huntington's disease, and pain, and the
 CC cardiovascular disorder is selected from congestive heart failure and
 CC myocardial infarction. The present sequence represents a human lysosomal
 CC acid lipase protein of the invention, the gene encoding this protein is
 CC located on human chromosome 10.

XX Sequence 311 AA;

Query Match 51.8%; Score 1108; DB 23; Length 311;

Best Local Similarity 58.7%; Pred. No. 7.9e-103;

Matches 229; Conservative 11; Mismatches 32; Indels 118; Gaps 8;

Qy 1 MWLLLTTCICGLNAGGFLDLENVPEVMMNTSEIIYNGYPSSEYEVTTEDGYIL 60

Db 30 MWLLLTTCICGLNAGGFLDLENVPEVMMNTSEIIYNGYPSSEYEVTTEDGYIL 89

Qy 61 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGLADAGYVMMGNSR 120

Db 90 LVNRIPYGRTHARSTGPRPVVYQHALFADNAYWLENYANGSLGLADAGYVMMGNSR 149

Qy 121 GNTWSRRHKTLSSETDEKFWAFSDEMAYDLPGVIDFVKNVGOEKLYFGHSLGTTIGF 180

Db 150 GNTWSRRHKTLSSETDEKFWAFRYTKG-----NAT----- 179

Qy 181 VAFSTMPPELAQRKMNPFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFLEDEKKT 240

Db 180 -----AERAKOMEPGP----- 191

Qy 241 IASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTGGSVNHLIKOLYH 300

Db 192 -----YWAIVDARESPFLFGNRE-----ESR-----GLKNT----- 217

Qy 301 SDEFRAVDGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHDVLTGTPQDVARILPQIK 360

Db 218 ---QAYDWGNDADNMKHYNOSHPPYIDLTAMKVPTAIWAGGHDVLTGTPQDVARILPQIK 273

Qy 361 SLSLVLSLLPEWEPTFDVFWGLDAPQRMFS 390

Db 274 SLH-YFKLLPDWN-HFDVFWGLDAPQRMYS 301

RESULT 7

AAO18227

ID AAO18227 standard; Protein; 392 AA.

XX AAO18227;

AC AAO18227;

DT 18-SEP-2002 (first entry)

XX Human lysosomal acid lipase related protein.

XX Human; lysosomal acid lipase; chromosome 10; lipemic; Wolman disease;
KW cholesteryl ester storage disease.
OS Homo sapiens.
XX US6387680-B1.
PN 14-MAY-2002.
XX 29-MAR-2001; 2001US-0820001.
PF 29-MAR-2001; 2001US-0820001.
PR (PEKE) PE CORP NY.
XX Merkulov GV, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2002-478445/51.
XX Isolated nucleic acids encoding a lysosomal acid lipase protein useful
PT for the prevention, diagnosis and treatment of severe infantile-onset
PT Wolman disease and late-onset cholesteryl ester storage disease -
XX Disclosure; Column 57-60; 68pp; English.
XX The present invention provides the protein, coding and genomic sequences
CC of a human lysosomal acid lipase. The sequences can be used in the
CC identification of modulators of lipase activity in cells and tissues that
CC express the lipase, particularly the severe infantile-onset Wolman
CC disease and the milder late-onset cholesteryl ester storage disease
CC (CESD), which are caused by mutations in different parts of the lysosomal
CC acid lipase (LIPA) gene. The present sequence is a protein shown in the
CC exemplification of the invention.
XX
XX Sequence 392 AA;

Query Match 51.3%; Score 1097; DB 23; Length 392;
Best Local Similarity 53.6%; Pred. No. 1.4e-101;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTNAGGFLDENENPEVNMNTSEIIYNGYPSEEVETEDGYILL 61
Db 1 MRFLGLVCLVWLTHSEGGGKLTAVDPETNMNVSEIIYNGYFFSEELVETEDGYILL 60
QY 62 VNRIPIYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 61 LNRIPGRKNSDKGPKPVVFLQHLGLADSSNWNVTNLANSSLGFLADAGYDVWNGNSRG 120
QY 122 NWSRRHKLTSETDEKFWAFSDEMAKYDLPQVIDPINKVTQOEKLYFTGHSLGTTIGFV 181
Db 121 NWSRRHKLTSLVSQDEFWAFSDEMAKYDLPASINFLNKTGQEQVYVYGHSGQTTIGFI 180
QY 182 AFSTWPELAQRKMNPFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKKTKI 241
Db 181 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLKDLFGDEFLPQSAFLKW 240
QY 242 ASTKICNNKILMLICEFMSLWAGSNKKNNQSRMDVYMSHAPTSVSSVHNILHIKOLYHS 301
Db 241 LGTHVCTHVILKELCNLCFLCGFNERNLNMSRDVYTHSPAGTSVQNMLHWSQAVKF 300
QY 302 DEFRAVDGNDADNMKHYNQSHPPYDILTKAMKVPYTAIWAGGHDVLTGTPDVARILPQIKS 361
Db 301 QKFOAFDWGSSAKNYFHYNQSPPTYNVKDMLVPTAVWSGGHDWLDVYDVNILLTQITN 360
QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGNHL 395
Db 361 LVFHES-IPWEH-HLDFIWLGDAPWRLYNIINL 392

RESULT 8
AAB90783
ID AAB90783 standard; Protein; 399 AA.

XX AAB90783;
XX 15-JUN-2001 (first entry)
XX Human shear stress-response protein SEQ ID NO: 66.
XX Human; shear stress-response protein; vascular disease;
KW arteriosclerosis.
XX Homo sapiens.
XX WO200125427-A1.
XX 12-APR-2001.
XX 02-OCT-2000; 2000WO-JP06840.
XX 01-OCT-1999; 99JP-0280976.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (NOJI/) NOJIMA H.
XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX WPI; 2001-266308/27.
XX N-PSDB; AAH02906.
XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
XX
XX Claim 60; Page 402-404; 678pp; Japanese.
XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
XX Sequence 399 AA;

Query Match 51.1%; Score 1091; DB 22; Length 399;
Best Local Similarity 53.3%; Pred. No. 5.7e-101;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTNAGGFLDENENPEVNMNTSEIIYNGYPSEEVETEDGYILL 61
Db 3 MRFLGLVCLVWLTHSEGGGKLTAVDPETNMNVSEIIYNGYFFSEELVETEDGYILL 62
QY 62 VNRIPIYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 63 LNRIPGRKNSDKGPKPVVFLQHLGLADSSNWNVTNLANSSLGFLADAGYDVWNGNSRG 122
QY 122 NWSRRHKLTSETDEKFWAFSDEMAKYDLPQVIDPINKVTQOEKLYFTGHSLGTTIGFV 181
Db 123 NWSRRHKLTSLVSQDEFWAFSDEMAKYDLPASINFLNKTGQEQVYVYGHSGQTTIGFI 182
QY 182 AFSTWPELAQRKMNPFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKKTKI 241
Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLKDLFGDEFLPQSAFLKW 242
QY 242 ASTKICNNKILMLICEFMSLWAGSNKKNNQSRMDVYMSHAPTSVSSVHNILHIKOLYHS 301
Db 243 LGTHVCTHVILKELCNLCFLCGFNERNLNMSRDVYTHSPAGTSVQNMLHWSQAVKF 302
QY 302 DEFRAVDGNDADNMKHYNQSHPPYDILTKAMKVPYTAIWAGGHDVLTGTPDVARILPQIKS 361
Db 303 QKFOAFDWGSSAKNYFHYNQSPPTYNVKDMLVPTAVWSGGHDWLDVYDVNILLTQITN 362
QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGNHL 395

Db 363 LVFHEH-IPWEH-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 9

AA66061

ID AAB66061 standard; Protein; 399 AA.

AC AAB66061;

DT 30-MAR-2001 (first entry)

DE Human lysosomal acid lipase protein.

XX Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.

OS Homo sapiens.

PN WO200077239-A2.

PD 21-DEC-2000.

PF 24-MAY-2000; 2000WO-US14858.

PR 14-JUN-1999; 99US-0333159.

PA (MILL-) MILLENNIUM PHARM INC.

XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;

PI WPI; 2001-032313/04.

DR TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's disease.

XX Claim 8; Fig.6; 359pp; English.

CC The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT sequences of the present invention.

XX Sequence 399 AA;

Query Match 51.1%; Score 1091; DB 22; Length 399;

Best Local Similarity 53.3%; Pred. No. 5.7e-101;

Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPEVWMTSEIIYNGPSEYEVTTEDGYILL 61

Db 3 MRFLGVVCLVLPWLPSESGGKLTAVDPETNMNVSEIIYNGPSEYEVTTEDGYILC 62

Qy 62 VNRIYPYGRTHARSTGPRPVVYMOHALFADNAYWLENVAGFLGLADAGYDVMWNSRG 121

Db 63 LNRPHGKKNHSDGKPPVFLQGLGLADSSNWTNLANSLGFLGLADAGYDVMWNSRG 122

Qy 122 NTSRRHKTSETDEKFWAFSDEMAYDLPGVDFIVNKTGOBKLYFIGHSLGTTIGV 181

Db 123 NTSRRHKTSETDEKFWAFSDEMAYDLPASINFILNKTGOEQVYVGHSGQTTIGFI 182

Qy 182 AFSTMPELAORIKMNFALGPTISFKYPTGIFTRFFLLPNSIIKAVGKGFLEDKTKKI 241

Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLPDHLKDLFGDKKEFLPQSAFLKW 242

Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTSSVHNILHIKQLYHS 301

Db 243 LGTHVCTHVLKELCGNLCLFCFLCGFNERNLNSRDVYVTHSPAGTSVQNMLHWSQAVKF 302

Qy 302 DEFRAIDMGNDADNMKHNQSHPPYIDLTAMKVPYTAIWAGGHVLTGTFQDVAVARILPQKKS 361

Db 303 QKFOAFDWGSSAKNYFHYNQSPPTNYKMDLVPYAVMSGGHDLADYVDVNNILLTQITN 362

Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQPMFSGNHL 395

Db 363 LVFHEH-IPWEH-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 10

AA660724

ID AAP60724 standard; Protein; 398 AA.

AC AAP60724;

DT 08-JUN-1991 (first entry)

DE Sequence of pregastric lipase.

XX Precursor polypeptide; secretion vector; enzyme.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= signal

XX Protein 20..398

PN WO8603778-A.

PD 03-JUL-1986.

XX 23-DEC-1985; 85WO-GB00599.

XX 21-DEC-1984; 84GB-0032483.

PR 23-DEC-1985; 85WO-GB00599.

PR 01-JAN-1986; 86GB-0019568.

XX (BREW-) BREWING RES FOUND.

PA (TUBB/) TUBB R S.

XX Tubb RS;

XX WPI; 1986-182910/28.

DR N-PSDB; AAN60685.

XX New precursor polypeptide of defined sequence - and corresp. DNA used to transform hosts for prodn. of the polypeptide

PT Example; Fig 5; 60pp; English.

PS The inventors claim a DNA sequence encoding AAP60723 linked to a promoter upstream and a gene for a polypeptide downstream.

CC Particular examples are the yeast enzyme AMG, the mammalian enzyme, gastric lipase and the mammalian lymphokine, interferon-alpha2.

XX Sequence 398 AA;

Query Match 49.2%; Score 1052; DB 7; Length 398;

Best Local Similarity 50.4%; Pred. No. 4.8e-97;

Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLAGGFLDLENEVNPVWMTSEIIYNGYPSSEYEVTTEDGYILL 61
 Db 1 MWLLTMAISLVLTGTHGLFGLKHPGSPVWNTNISMITYWGYPNEEYEVTTEDGYILE 60
 QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADADGYVWNGNSRG 121
 Db 61 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADADGYVWNGNSRG 120
 QY 122 NTSRRHKLSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 181
 Db 121 NTSRRHKLSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 180
 QY 182 AFSTMPPELAQRKIMNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIFGDKIFYPHNFFDQF 240
 QY 242 ASTKICNNKILWLCSEFSLWAGSNKKNNQSRMDVYKSHAPTSVSHNHLHIKOLYHS 301
 Db 241 LATEVCSREMLNLCSNALFIICGFSKNTSRLDVLVLSHNPAGTSVQNMFWHTQAVKS 300
 QY 302 DEFRAVDWGNADNMKHYNOSHPIYDLTAMKVPTAIWAGGHVDVLTGTPDVARILPOIKS 361
 Db 301 GKFQAYDWGSPVQNRMHYDOSPPYNTAMNVPYIAVWNGGRDLLADPDQVGLLLPKLPN 360
 QY 362 LSLVLSLLPEWETFDVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWAMDAPQEVYN 387

RESULT 11

AAW06058
 ID AAP06058 standard; Protein; 398 AA.
 AC AAW06058;
 DT 22-AUG-1991 (first entry)
 XX Sequence of human pregastric lipase.
 DE Cystic fibrosis therapy; enzyme; lipase deficiency.
 KW Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein 20..398
 PN W08601532-A.
 XX 13-MAR-1986.
 XX 15-AUG-1985; 85WO-GB00364.
 XX 21-AUG-1984; 84GB-0021210.
 PR 15-AUG-1985; 85WO-GB00364.
 PR 01-JAN-1986; 86GB-0008897.
 XX (CELL-) CELYTECH LTD.
 PA (LOWE/) LOWE P A.
 XX Lowe PA;
 XX WPI; 1986-081634/12.
 DR N-PSDB; AAN60566.
 XX New gastric lipase protein, esp. of human origin - for treating
 PT lipase deficiency, and DNA sequences coding for it
 XX Disclosure; Fig 3; 39pp; English.
 PS The inventors claim a pregastric lipase protein and a gene encoding
 CC it. Gastric lipase protein is useful for oral administration to
 CC treat lipase deficiency, e.g. cystic fibrosis or pancreatitis.

XX SQ Sequence 398 AA;
 Query Match 49.2%; Score 1052; DB 7; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
 QY 2 MWLLTTTCLICGTLAGGFLDLENEVNPVWMTSEIIYNGYPSSEYEVTTEDGYILL 61
 Db 1 MWLLTMAISLVLTGTHGLFGLKHPGSPVWNTNISMITYWGYPNEEYEVTTEDGYILE 60
 QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADADGYVWNGNSRG 121
 Db 61 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADADGYVWNGNSRG 120
 QY 122 NTSRRHKLSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 181
 Db 121 NTSRRHKLSETDEKFWAFSPDEMAKYDLPVGVDFIVNKTGOEKLFFIGHSLGTTIGFV 180
 QY 182 AFSTMPPELAQRKIMNFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIFGDKIFYPHNFFDQF 240
 QY 242 ASTKICNNKILWLCSEFSLWAGSNKKNNQSRMDVYKSHAPTSVSHNHLHIKOLYHS 301
 Db 241 LATEVCSREMLNLCSNALFIICGFSKNTSRLDVLVLSHNPAGTSVQNMFWHTQAVKS 300
 QY 302 DEFRAVDWGNADNMKHYNOSHPIYDLTAMKVPTAIWAGGHVDVLTGTPDVARILPOIKS 361
 Db 301 GKFQAYDWGSPVQNRMHYDOSPPYNTAMNVPYIAVWNGGRDLLADPDQVGLLLPKLPN 360
 QY 362 LSLVLSLLPEWETFDVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWAMDAPQEVYN 387
 RESULT 12
 AAW09383
 ID AAW09383 standard; Protein; 398 AA.
 AC AAW09383;
 DT 19-AUG-1997 (first entry)
 XX Human gastric lipase protein sequence.
 DE Duodenal; gastric; lipase; transgenic; plant; recombinant; extract;
 KW food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy;
 KW hydrolysis; trans-esterification; substrate; enzyme; biofuel; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note="signal peptide"
 FT Protein /note="mature protein"
 XX W09633277-A2.
 PN 24-OCT-1996.
 PD 19-APR-1996; 96WO-FR00606.
 XX 20-APR-1995; 95FR-0004754.
 PR (BIOC-) BIOCEM SA.
 PA (LJOU) INST RECH JOUVEINAL.
 XX Baudino S, Benicourt C, Cudrey C, Gruber V, Lenee P;
 PI Merot B;
 XX WPI; 1996-485783/48.

DR N-PSDB; AAT58916.
 XX Recombinant human or canine pre-duodenal lipase prodn. in transgenic
 PT plants - useful for facilitating absorption of fat, as bio-catalysts
 PT and for prodn. of bio-fuel
 XX
 XX Claim 3; Fig 5; 130pp; French.
 XX
 CC This is the amino acid sequence of the human pre-duodenal (i.e. gastric)
 CC lipase enzyme. The sequence can be used to generate transgenic plants
 CC producing recombinant lipase in an enzymatically active form.
 CC Alternatively amino acids 20-23 or 20-73 (1-4 or 1-54 of the mature
 CC protein, respectively) can be deleted to form the derivatives designated
 CC delta-4 or delta-54 respectively. Plants, or their extracts, expressing
 CC the lipases or the truncated derivatives, can be used:
 CC (a) as pharmaceuticals or food to facilitate absorption of fat, either
 CC in healthy subjects or in patients with inadequate levels of
 CC gastric/pancreatic lipase e.g. those with cystic fibrosis or exocrine
 CC pancreatic insufficiency, in the elderly or in patients undergoing medical
 CC treatment which alters fat adsorption; (b) for performing industrial or
 CC agricultural reactions, e.g. in processing of fats or in the dairy
 CC industry, for hydrolysis or transesterification reactions, etc., where
 CC the plant material may provide both enzyme and substrate. The transgenic
 CC plants can also be used for biofuel production.
 XX
 SQ Sequence 398 AA;

Query Match 49.2%; Score 1052; DB 17; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;
 Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVPVMMNTSEIIYNGYSEYEVTTEDGYILL 61
 Db 1 MWLLTMSLISVLGTTGHLFGKLPSPVMTNISQMTIYWGYPNEEVVTDGYILE 60
 Qy 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRKNSGNTGQRPVFLQHGLLASATNWSLNPNLSLAFTLADAGYDVMGNSRG 120
 Qy 122 NWSRRHKTLSBDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
 Db 121 NTSARRNLVSPDSVEFWAFSDEMAYDLPATIDFIVKTKGQKQLHVHSGQTIGFI 180
 Qy 182 AFSTMPLEAQRKIMNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIDGKIFVPHNFFDQF 240
 Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNQSDMDVYMSHAPTSSVHNILHIKQLYHS 301
 Db 241 LATEVCSREMLNLLCSNALFTICGDSKNFNTSRDLYVLSHNPAGTSVQNMFHWTQAVKS 300
 Qy 302 DEFRAIDWGNADNMKNHYNQSHPIYDITAMKVPTAIWAGGHDVLGTPQDVARILPOIKS 361
 Db 301 GKQAYDNGSPQVRMHYDQSPPYNYVTAMNPIAVWNGKDLADPDQVGLLLPKLPN 360
 Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
 Db 361 L-IYHKEIPFYN-HLDFIWMADAQEVZN 387

RESULT 13
 AAB66086
 ID AAB66086 standard; protein; 398 AA.
 AC AAB66086;
 XX
 XX 30-MAR-2001 (first entry)
 DT Human lipase protein.
 XX
 DE Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;
 KW central nervous system; focal brain disorder; bipolar affective disorder;
 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;
 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
 KW neuropsychiatric; psychoactive substance use; anxiety.
 OS Homo sapiens.
 XX
 XX WO200077239-A2.
 PN
 XX 21-DEC-2000.
 PD
 XX 24-MAY-2000; 2000WO-US14858.
 PF
 XX 14-JUN-1999; 99US-0333159.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX McCarthy SA, Fraser CC, Sharp JD, Barnes TM;
 PI WPI; 2001-032313/04.
 XX
 DR TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for
 XX screening assays and diagnostic assays and for the treatment of
 PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's
 PT disease -
 PT
 XX
 PS Disclosure; Fig 6; 359pp; English.

XX The present invention relates to TANGO or INTERCEPT proteins and coding
 CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,
 CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding
 CC sequences are useful for the treatment of neurological disorders such as
 CC central nervous system (CNS) disorders, CNS-related disorders, focal
 CC brain disorders, global-diffuse cerebral disorders and other
 CC neurological and cerebrovascular disorders. The CNS disorders include
 CC Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
 CC lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome,
 CC autonomic function disorders such as hypertension and sleep disorders,
 CC neuropsychiatric disorders, psychoactive substance use disorders,
 CC anxiety, and bipolar affective disorder. The present sequence is a
 CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT
 CC sequences of the present invention.

SQ Sequence 398 AA;

Query Match 49.2%; Score 1052; DB 22; Length 398;
 Best Local Similarity 50.4%; Pred. No. 4.8e-97;
 Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVPVMMNTSEIIYNGYSEYEVTTEDGYILL 61
 Db 1 MWLLTMSLISVLGTTGHLFGKLPSPVMTNISQMTIYWGYPNEEVVTDGYILE 60
 Qy 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
 Db 61 VNRIPYGRKNSGNTGQRPVFLQHGLLASATNWSLNPNLSLAFTLADAGYDVMGNSRG 120
 Qy 122 NWSRRHKTLSBDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
 Db 121 NTSARRNLVSPDSVEFWAFSDEMAYDLPATIDFIVKTKGQKQLHVHSGQTIGFI 180
 Qy 182 AFSTMPLEAQRKIMNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTKI 241
 Db 181 AFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVQSLFKFIDGKIFVPHNFFDQF 240
 Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNQSDMDVYMSHAPTSSVHNILHIKQLYHS 301
 Db 241 LATEVCSREMLNLLCSNALFTICGDSKNFNTSRDLYVLSHNPAGTSVQNMFHWTQAVKS 300
 Qy 302 DEFRAIDWGNADNMKNHYNQSHPIYDITAMKVPTAIWAGGHDVLGTPQDVARILPOIKS 361
 Db 301 GKQAYDNGSPQVRMHYDQSPPYNYVTAMNPIAVWNGKDLADPDQVGLLLPKLPN 360
 Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMFS 390

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| : :| : ||:| :||| ::
361 L-IYHKEIPFYN-HLDFIWAMDAPOEYVN 387
Db

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RESULT 14

AAE11931
ID AAE11931 standard; Protein; 409 AA.

XX
AC AAE11931;

XX
DT 18-DEC-2001 (first entry)

XX	DE	Human CG162 (or C59) lipase protein #2.
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100	100	100

XX Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
KW cardiovascular disease; lipid metabolism; myocardial infarction;
KW cerebral ischaemia; arterial thrombosis; thrombolytic; antiplatemic;
KW coronary artery thrombosis; cerebral artery thrombosis; stroke;
KW intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
KW neuroprotectant; cerebroprotective.

XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
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FT Peptide
FT 1..19
   /label= signal_peptide
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FT	Protein	20..409
FT		/note=

XX PN WO200179446-A2.

XX
PD 25-OCT-2001.

XX
PF
16-APR-2001;

XX
PR 14-APR-2000; 2000US-197137P.

PR 20-JUN-2000; 2000US-0598042.
PR 03-AUG-2000; 2000US-0631451.

PR 22-SEP-2000; 2000US-0667298,
PR 17-NOV-2000; 2000US-0714936.

XX
PA (HYSE-) HYSEQ INC.XX
PI Ballinger DG, Loeb D, Mont

PI Liu C, Asundi V, Zhao QA,
PI Wang D;

XX
DR WPI; 2001-611724/70.

DR N-PSDB; AAD19226.
XX

PT Nucleic acids encoding
PT receptor polypeptide

lipid metabolism dis

PS
XX

CC The invention relates
CC CG95, CG121, CG162,

CC involved in lipid metabolism and cardiovascular disease such as human
CC apolipoproteins, lipases and lipoprotein receptor proteins. These DNA

CC and protein sequences are useful for treating or preventing disorders
CC associated with apolipoproteins, lipases and lipoprotein receptor (ALL

CC expression and for treating lipid metabolism, cardiovascular diseases
CC and thrombosis. Antibodies against these proteins are useful for

CC determining the presence of or p
CC with altered levels of these' seq

useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLr proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular

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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:34:17 ; Search time 19 seconds
(without alignments)
1270.986 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLTTTCLICGTLNAGG.....PDFVWGLDAPQMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	2137	100.0	395	12 US-10-003-302-2
2	2030	95.0	398	9 US-10-056-744B-2
3	1097	51.3	392	12 US-10-003-302-4
4	1091	51.1	399	9 US-10-042-431-41
5	1091	51.1	399	9 US-09-759-130B-411
6	1052	49.2	398	9 US-10-042-431-75
7	1052	49.2	398	9 US-09-759-130B-445
8	1031	48.2	409	10 US-09-835-996A-21
9	1031	48.2	423	9 US-10-042-431-47
10	1031	48.2	423	9 US-09-759-130B-417
11	1023	47.9	390	9 US-10-042-431-49
12	1023	47.9	390	9 US-09-759-130B-419
13	995	46.6	374	10 US-09-811-825-4
14	995	46.6	398	10 US-09-811-825-2
15	700	32.8	221	9 US-10-042-431-50
16	700	32.8	221	9 US-09-759-130B-420
17	341	16.0	127	9 US-10-056-744B-5
18	297	13.9	144	9 US-10-042-431-52
19	297	13.9	144	9 US-09-759-130B-422

20	111	5.2	297	12	US-10-080-644-7	Sequence 7, Appli
21	96	4.5	262	9	US-10-027-800-35	Sequence 35, Appl
22	96	4.5	262	9	US-10-027-800-35	Sequence 35, Appl
23	96	4.5	262	10	US-09-903-410-35	Sequence 35, Appl
24	94.5	4.4	305	10	US-09-815-242-12337	Sequence 12337, A
25	90.5	4.2	222	10	US-09-815-242-5276	Sequence 5276, Ap
26	90	4.2	286	10	US-09-950-368-9	Sequence 9, Appli
27	89.5	4.2	494	9	US-10-066-500-139	Sequence 139, App
28	89.5	4.2	494	9	US-10-066-500-139	Sequence 139, App
29	89.5	4.2	494	9	US-10-066-273-139	Sequence 139, App
30	89.5	4.2	494	9	US-10-066-494-139	Sequence 139, App
31	89.5	4.2	494	9	US-10-066-269-139	Sequence 139, App
32	89.5	4.2	494	9	US-10-066-193-139	Sequence 139, App
33	89.5	4.2	494	9	US-10-066-211-139	Sequence 139, App
34	89	4.2	297	9	US-10-027-800-37	Sequence 37, Appl
35	89	4.2	297	9	US-10-027-800-37	Sequence 37, Appl
36	89	4.2	297	10	US-09-903-410-37	Sequence 37, Appl
37	87.5	4.1	480	10	US-09-881-752A-38	Sequence 38, Appl
38	86.5	4.0	341	10	US-09-799-777-61	Sequence 61, Appl
39	86.5	4.0	441	10	US-09-729-402-8	Sequence 8, Appli
40	86.5	4.0	564	9	US-09-944-160-12	Sequence 12, Appl
41	86	4.0	1183	9	US-09-870-759-45	Sequence 45, Appl
42	85	4.0	678	9	US-09-738-626-6025	Sequence 6025, Ap
43	84.5	4.0	770	9	US-09-992-896-9	Sequence 9, Appli
44	83.5	3.9	770	10	US-09-815-656-31	Sequence 31, Appl
45	83	3.9	719	9	US-10-234-266-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-003-302-2
; Sequence 2, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003.302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-2

Query Match	100.0%	Score	2137;	DB	12;	Length	395;
Best Local Similarity	100.0%	Pred. No.	1.6e-204;				
Matches	395;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MMWLLTTTCLICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYL	60				
Db	1	MMWLLTTTCLICGTLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEVTTEDGYL	60				
Qy	61	LVNRIPTYGRTHARSTGPRPVVYMQHALFADNAYWLENANGSLGFLADAGYDVMGNSR	120				
Db	61	LVNRIPTYGRTHARSTGPRPVVYMQHALFADNAYWLENANGSLGFLADAGYDVMGNSR	120				
Qy	121	GNTWSRRKTLTSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTCF	180				
Db	121	GNTWSRRKTLTSETDEKFWAFSDEMAYDLPGVDFIVNKTGQEKLYFIGHSLGTTCF	180				
Qy	181	VAFTMPLEAORIKMNFALGPTISFKYPTGIFTRFLLPNSITIKAVFGTKGFLEDDKTK	240				
Db	181	VAFTMPLEAORIKMNFALGPTISFKYPTGIFTRFLLPNSITIKAVFGTKGFLEDDKTK	240				
Qy	241	IATKICNKKIWLITCSBFMSLWAGSNKKNMQSMDVMYMSHAPTGSVVHNTLHKLYH	300				
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QY 301 SDEFRAYDGNADNKKHYNQSHPPYDILTAMKVPTAIWAGHDVLTGPQDVVARILPOIK 360
Db 301 SDEFRAYDGNADNKKHYNQSHPPYDILTAMKVPTAIWAGHDVLTGPQDVVARILPOIK 360
QY 361 SLSVLSSLPEWEPTDFVWGLDAPQRMFSGHNHL 395
Db 361 SLSVLSSLPEWEPTDFVWGLDAPQRMFSGHNHL 395
RESULT 2
US-10-056-744B-2
; Sequence 2, Application US/10056744B
; Publication No. US20020193303A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL ESTER
; FILE OF INVENTION: HYDROLASE AND USES THEREFOR
; FILE REFERENCE: MPI2001-026PRNM
; CURRENT APPLICATION NUMBER: US/10/056,744B
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/264,167
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-744B-2
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Best Local Similarity 97.2%; Pred. No. 7.1e-194;
Matches 379; Conservative 2; Mismatches 7; Indels 2; Gaps 2;
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QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENANGSLGFLADAGYDVMGNSR 120
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QY 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPVGFIDFVNTKGQKLYFIHSLGTTIGF 180
Db 121 GNTWSRRHKTSETDEKFWAFSDEMAKYDLPVGFIDFVNTKGQKLYFIHSLGTTIGF 180
QY 181 VAFSTWPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
Db 181 VAFSTWPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTK 240
QY 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMNOSRMDVYMSHAPTGSVVHNLHKLQYH 300
Db 241 IASTKICNNKILWLICSEFMSLWAGSNKKNMNOSRMDVYMSHAPTGSVVHNLHKLQYH 300
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RESULT 3
US-10-003-302-4
; Sequence 4, Application US/10003302
; Patent No. US20020142435A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01186DIV
; CURRENT APPLICATION NUMBER: US/10/003,302
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-302-4
Query Match 51.3%; Score 1097; DB 12; Length 392;
Best Local Similarity 53.6%; Pred. No. 5.5e-107;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;
QY 2 MWMLLTTCICGLNAGGFLDLENEVPEVMMNTSEIIYNGYPSEYEYVTTEDGYILL 61
Db 1 MRFLGLVWLVLWTLHSEGGKLTAVDPETNMNVSEIISYWGFPSEYLVETEDGYILC 60
QY 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENANGSLGFLADAGYDVMGNSRG 121
Db 61 LNRIPHGRKNHSDKGPVVFLOHGLLADSSNWNVTNLANSSLGFLADAGFDVWGNRSRG 120
QY 122 NTWSRRHKTSETDEKFWAFSDEMAKYDLPVGFIDFVNTKGQKLYFIHSLGTTIGFV 181
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QY 182 AFTWPELAQRIKNNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDDKTKI 241
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QY 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMNOSRMDVYMSHAPTGSVVHNLHKLQYHS 301
Db 241 LGTHVCTHVLKELCNLCFLCFCGFEENLNMSRVDVYTTHTSPAGTSYQNMLHWSQAVKF 300
QY 302 DEFAYDGNADNKKHYNQSHPPYDILTAMKVPTAIWAGHDVLTGPQDVVARILPOIKS 361
Db 301 QKQFAFDGSSAKNTFHYNQSPYPTYNKMDLVPTAVMSGHDLADYDVNILLTQITN 360
QY 362 LSLVLSSLPEWEPTDFVWGLDAPQRMFSGHNHL 395
Db 361 LVFHES-IPWE-HLDFWGLDAPWRLNKIINL 392
RESULT 4
US-10-042-431-41
; Sequence 41, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 53.3%; Pred. No. 2.2e-100;

Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVNPVMMNTSEIIYNGYPSSEYEVETEDGYILL 61
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Qy 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
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Qy 242 ASTKICNNKILWICSEFMSLWAGSNKKNQSDVYMSHAPTSSVHNILHIKOLYHS 301
Db 243 LGTHVCTHVILKELCGNLCFLCGFNERNLNNSRDVYVTHSPAGTSVQNNMLHWSQAVKF 302
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Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGHNHL 395
Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 5
US-09-759-130B-411
; Sequence 411, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350MNI
; CURRENT APPLICATION NUMBER: US/09759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707

; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-411

Query Match 51.1%; Score 1091; DB 9; Length 399;
Best Local Similarity 53.3%; Pred. No. 2.2e-100;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVNPVMMNTSEIIYNGYPSSEYEVETEDGYILL 61
Db 3 MRFLGLVCLVLPVHSGSGKLTAVDPETNMNVEIISYWGFFSEYLVETEDGYILC 62
Qy 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 63 LNRIPHGRKNHSDKPKPVVFLQGLLADSSNWNVTNLANSLSGLFLADAGFDVWNGNSRG 122
Qy 122 NTWSRHHKTLSETDEKFWAFSDENAKYDLPQVDFVYKTCGOEKLIFIGHSLGTIGFV 181
Db 123 NTWSRHHKTLVSQDEFWAFSDENAKYDLPASINFILNKTCGOEYVYVGHSGQTTIGFI 182
Qy 182 AFSTPELAQRKIMNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 183 AFSQIPELAKRIKMFALGPVAVAFCTSPMAKLGRLDPHLIKDLFGDKEFLPQSAFLKW 242
Qy 242 ASTKICNNKILWICSEFMSLWAGSNKKNQSDVYMSHAPTSSVHNILHIKOLYHS 301
Db 243 LGTHVCTHVILKELCGNLCFLCGFNERNLNNSRDVYVTHSPAGTSVQNNMLHWSQAVKF 302
Qy 302 DEFRAIDGNDADNMKNHYNQSHPPYDLTAMKVPYTAIWAGGHDVLTGTPQDVARILPOLKS 361
Db 303 QKQAFDNGSSAKNFYHNSYPTTYNVKMDLVPYAVWSGGHDLADYVDVNNILLTQITN 362
Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFSGHNHL 395
Db 363 LVFHES-IPWE-HLDFIWLGLDAPWRLYNKIINL 394

RESULT 6
US-10-042-431-75
; Sequence 75, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-75

Query Match 49.2%; Score 1052; DB 9; Length 398;
Best Local Similarity 50.4%; Pred. No. 1.7e-96;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTNLNAGGFLDLENEVNPVMMNTSEIIYNGYPSSEYEVETEDGYILL 61

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; SEQ ID NO 445
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-445

Query Match          49.2%; Score 1052; DB 9; Length 398;
Best Local Similarity 50.4%; Pred. No. 1.7e-96;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps

Qy      2 MWLLTTTCLICGTLNAGGFLDLENEYPEVMMNTSEIIYNGYPSYEVTTEDGYILL 61
Db      1 MWLLTMAISLVLTGTHLFGKLUHGPSPVYTMISQIYWGYPNEYEVVTTEDGYILE 60

Qy      62 VNRIPYGRTHARSTGRPPVVMYMQHALFNADNAYWLENYANGSLGFLLDAGYDVMMGNSRG 121
Db      61 VNRIPYCKKNSGTGRPVVFLQHGLLASATNWTISNLNPLAFILADAGYDVWLGNRSRG 120

Qy      122 NTVSRRHKTISETDEKFWAFSDFEMAKYDLPVGFIDFVTKTQGBKLYFIHGSLGTTTGFV 181
Db      121 NTWARRNLYYSPDSVEFWAFSDFEMAKYDLPATIDFVTKTKQKQLHYVGHSGQTTTIGFI 180

Qy      182 AFSTMPLEAQRKMNFAFGTISFKYPTGTFTRFFLLPNSIIRKAVFCTKGFFLEDKTKKI 241
Db      181 AFSTNPSLAKRIKTFYALAPVATVTKYTKSLINKLRFVQSLFKPIFGDKIFYPHNFTDQF 240

Qy      242 ASTKICNKKTLWLICSEFMSLWAGSNKKMNQSRMDYVMSHAPTGSVHNHILHIKQLYHS 301
Db      241 LATEVCSREMLNLCSNALFIICGFSKFNFTSELDVYLSHNPACTSVQNMFHTQAVKS 300

Qy      302 DEFRAVDWGADNANKMHYNQSHPHPIYDLTAMKVPTAIWAGGHVDVLGTPQDVARILPOIKS 361
Db      301 GKFAQYDWGSPVQNRMHYDQSPPPYVNTAMNVPYIAVWNGGKDLLADPQDVGVLPLKLPN 360

Qy      362 LSLVLSLLPWEPTFFDFVWGLDAPQRMFS 390
Db      361 L-IYHKEIPFYN-HLDFIWAMDAPQEYIN 387

RESULT 8
US-09-835-996A-21
; Sequence 21, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyao
; APPLICANT: Qian, Xiaohong
; APPLICANT: Wang, Dunrui
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45

```

SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 409
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-996A-21

Query Match 48.2%; Score 1031; DB 10; Length 409;
Best Local Similarity 51.0%; Pred. No. 2.2e-94;
Matches 199; Conservative 61; Mismatches 124; Indels 6; Gaps 4;

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QY 2 MWLLTTTCLICGTLNACGFLDLENE-VNPEVWMTSEIIYNGVPSEYEVTTEDGYIL 60
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 3 MWLLLVAYMFQFNVNS---VHMPTKAYDPEAFNMNISEIIHQGYPCPEYEVATEDGYIL 59
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGDVVMGNSR 120
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 60 SVNRIPRGLVQPKTGRPVLLQHLGVLGGASNWNISLNPNNLSGLFADAGFDVVMGNSR 119
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 121 GNTWSRRHKTSETDEKFWAFSDFEMAKYDLPVGIDFIVNKTGQEKLYFIGHSLGTTICF 180
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 120 GNWSRKHKTLSIDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYVVGYSQGTMGF 179
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 181 VAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 180 IAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 241 IASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTGVSSVHNILHIKOLYH 300
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 240 QLVYILCGQVILDQICSNIMLLGGFNTNNMNSRASVYAHTLAGTSVQNLHWSQAVN 299
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 301 SDEFRAYDNGDADNMKNHYNOSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVVARILPQIK 360
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 300 SGELRAFDWGSETKLEKCNQPTPVRYRVRDVTPTAMWTGGQDWLSNPEDVKMLLSEVT 359
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 361 SLSLVLSLLPEWEPTFFDFVWGLDAPQRMFS 390
   :|| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 360 NL-IYHKNIPWEAHV-DFIWLGLDAPHRYN 387
   :|| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

RESULT 9

US-10-042-431-47
Sequence 47, Application US/10042431
Publication No. US20020182675A1
GENERAL INFORMATION:
APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-6U2
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 423
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-431-47

Query Match 48.2%; Score 1031; DB 9; Length 423;
Best Local Similarity 51.0%; Pred. No. 2.3e-94;
Matches 199; Conservative 61; Mismatches 124; Indels 6; Gaps 4;

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QY 2 MWLLTTTCLICGTLNACGFLDLENE-VNPEVWMTSEIIYNGVPSEYEVTTEDGYIL 60
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 17 MWLLLVAYMFQFNVNS---VHMPTKAYDPEAFNMNISEIIHQGYPCPEYEVATEDGYIL 73
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

```
QY 61 LVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGDVVMGNSR 120
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 74 SVNRIPRGLVQPKTGRPVLLQHLGVLGGASNWNISLNPNNLSGLFADAGFDVVMGNSR 133
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 121 GNTWSRRHKTSETDEKFWAFSDFEMAKYDLPVGIDFIVNKTGQEKLYFIGHSLGTTICF 180
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 134 GNWSRKHKTLSIDQDEFWAFSYDEMAREFDLPVINFILQKTGQEKIYVVGYSQGTMGF 193
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 181 VAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 240
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 194 IAFSTMPLELAQRIKKNFALGPTISFKYPTGIFTRFLLPNSLIKAVFGTKGFFLEDKTK 253
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 241 IASTKICNNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTGVSSVHNILHIKOLYH 300
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 254 QLVYILCGQVILDQICSNIMLLGGFNTNNMNSRASVYAHTLAGTSVQNLHWSQAVN 313
   :||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 301 SDEFRAYDNGDADNMKNHYNOSHPIYDLTAMKVPTAIWAGGHDVLGTPQDVVARILPQIK 360
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 314 SGELRAFDWGSETKLEKCNQPTPVRYRVRDVTPTAMWTGGQDWLSNPEDVKMLLSEVT 373
   ||||| : : : : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 361 SLSLVLSLLPEWEPTFFDFVWGLDAPQRMFS 390
   :|| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 374 NL-IYHKNIPWEAHV-DFIWLGLDAPHRYN 401
   :|| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

RESULT 10

US-09-759-1308-417
Sequence 417, Application US/097591308
Publication No. US20030022279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: MPI00-5350MIM
CURRENT APPLICATION NUMBER: US/09/759,1308
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 417
LENGTH: 423

Query Match 47.9%; Score 1023; DB 9; Length 390;
Best Local Similarity 53.4%; Pred. No. 1.3e-93;
Matches 194; Conservative 54; Mismatches 113; Indels 2; Gaps 2;

Qy 28 VNPVWMTSEIIYNGYPSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVYVMOHALFADNAYWLE 87
Db 8 VDPEAFMISEIIHQGYPCYEYEVATEDGYILSVNRIPRGVLQVQPKTGSRPVLLQHL 67
Qy 88 FADNAYWLENYANGSLGFLLDAGYDVWNGSRGNTWRRHKTLSETDEKFWAFSDEMA 147
Db 68 VCGASWISLNPNSLGFILADAGFDVWNGSRGNAWRKHKTLSDIDDEFWAFSYDEMA 127
Qy 148 KYDLPVIDFVNTKGKLYFIHSLGTTIGFVAFSTMPPELAQRIKMNFAALGPTISPKY 207
Db 128 RFDLPAVINFLQKTGQEKIYVYSGQTTMGFIATFSTMPPELAQRIKMYFALATPVKH 187
Qy 208 PTGIFTRFLLPNSLIKAVGTFKGFLEDDKTKIATSKICNNKILWLCSEFMSLWAGSN 267
Db 188 AKSPGTFKLLPDMMIKGLFKRKEFLYQTRFLQVLYLCGVILDDQICSNIMLLGGFN 247
Qy 268 KKNMOSRDVYMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKNHYNQSHPTIY 327
Db 248 TNNMNSRASVYAHTLAGTSVONILHWSQAVNSGELRAFDWGSSEKLNKCNQPTPVRY 307
Qy 328 DLTAMKVPATWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPTFFDVGDLAPOR 387
Db 308 RVRDMTPTAMWTGGDWSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 365
Qy 388 MFS 390
Db 366 MIN 368

RESULT 13
US-09-811-825-4
; Sequence 4, Application US/09811825
; Patent No. US20020144297A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811.825
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Human
US-09-811-825-4

Query Match 46.6%; Score 995; DB 10; Length 374;
Best Local Similarity 53.4%; Pred. No. 7.4e-91;
Matches 189; Conservative 52; Mismatches 111; Indels 2; Gaps 2;

Qy 37 SEIIYNGYPSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVYVMOHALFADNAYWLE 96
Db 1 SEIIHQGYPCYEYEVATEDGYILSVNRIPRGVLQVQPKTGSRPVLLQHLGVLGGASNMIS 60
Qy 97 NYANGSLGFLLDAGYDVWNGSRGNTWRRHKTLSETDEKFWAFSDEMAKYDLPGVID 156
Db 61 NLPNNSLGFILADAGFDVWNGSRGNAWRKHKTLSDIDDEFWAFSYDEMARFDLPVIN 120
Qy 157 FIVNKTGQEKLYFIHSLGTTIGFVAFSTMPPELAQRIKMNFAALGPTISFKYPTGIFTRFF 216
Db 121 FILQKTGQEKIYVYSGQTTMGFIATFSTMPPELAQRIKMYFALATPVKHAKSPGTFKL 180
Qy 217 LLPNSIIKAVGTFKGFLEDDKTKIATSKICNNKILWLCSEFMSLWAGSNKNNQSRM 276
Db 181 LLPDMMIKGLFKRKEFLYQTRFLQVLYLCGVILDDQICSNIMLLGGFNTNNMMSRA 240

Qy 277 DVYMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKNHYNQSHPTIYDLTAMKVPT 336
Db 241 SVYAHTLAGTSVONILHWSQAVNSGELRAFDWGSSEKLNKCNQPTPVRYRVRDMTVP 300
Qy 337 AIWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPTFFDVGDLAPORMFS 390
Db 301 AMWTGGDWSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 352

RESULT 14
US-09-811-825-2
; Sequence 2, Application US/09811825
; Patent No. US20020144297A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811.825
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Human
US-09-811-825-2

Query Match 46.6%; Score 995; DB 10; Length 398;
Best Local Similarity 53.4%; Pred. No. 8.1e-91;
Matches 189; Conservative 52; Mismatches 111; Indels 2; Gaps 2;

Qy 37 SEIIYNGYPSEYEVTEDGYILLVNRIPYGRTHARSTGPRPVYVMOHALFADNAYWLE 96
Db 25 SEIIHQGYPCYEYEVATEDGYILSVNRIPRGVLQVQPKTGSRPVLLQHLGVLGGASNMIS 84
Qy 97 NYANGSLGFLLDAGYDVWNGSRGNTWRRHKTLSETDEKFWAFSDEMAKYDLPGVID 156
Db 85 NLPNNSLGFILADAGFDVWNGSRGNAWRKHKTLSDIDDEFWAFSYDEMARFDLPVIN 144
Qy 157 FIVNKTGQEKLYFIHSLGTTIGFVAFSTMPPELAQRIKMNFAALGPTISFKYPTGIFTRFF 216
Db 145 FILQKTGQEKIYVYSGQTTMGFIATFSTMPPELAQRIKMYFALATPVKHAKSPGTFKL 204
Qy 217 LLPNSIIKAVGTFKGFLEDDKTKIATSKICNNKILWLCSEFMSLWAGSNKNNQSRM 276
Db 205 LLPDMMIKGLFKRKEFLYQTRFLQVLYLCGVILDDQICSNIMLLGGFNTNNMMSRA 264
Qy 277 DVYMSHAPTSSVHNILHIKOLYHSDFRAYDWGNDADNMKNHYNQSHPTIYDLTAMKVPT 336
Db 265 SVYAHTLAGTSVONILHWSQAVNSGELRAFDWGSSEKLNKCNQPTPVRYRVRDMTVP 324
Qy 337 AIWAGHDVLTGPQDVARILPOIKSLSLVLSLLPEWEPTFFDVGDLAPORMFS 390
Db 325 AMWTGGDWSNPEDVKMLLSEVTNL-IYHKNIPWAHV-DFIWGLDAPHRMYN 376

RESULT 15
US-10-042-431-50
; Sequence 50, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-602
; CURRENT APPLICATION NUMBER: US/10/042.431
; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-50

Query Match 32.8%; Score 700; DB 9; Length 221;
Best Local Similarity 61.0%; Pred. No. 8.1e-62;
Matches 128; Conservative 32; Mismatches 50; Indels 0; Gaps 0;
QY 28 VNPEVMMNTSEIIYNGYSPSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHAL 87
Db 8 VDPEAFMNISEIIHQGYPCSEYEVATEDGYILSVNRIPRGLVQPKTGSRPVLLQHGL 67
QY 88 FADNAYWLENYANGSLGFLLDAGYDVWNGSRGNTWSRRHKTLSETDEKFWAFSFDEMA 147
Db 68 VGGASWISNLPNNSLGFILADAGEDVWNGSRGNWSRKHKTLSDIDQDEFWAFSYDEMA 127
QY 148 KYDLPGVIDFVNVKGTQGEKLYFIGHSLGTTIGFVAFSTMPPELAQRKMNFMALGPTISFKY 207
Db 128 RFDLPAVINFIQKTQGEKLYYVGYSGTGTMGTFIAFSTMPPELAQRKIKMYFALAPIATVKH 187
QY 208 PTGIETRFELLPNSIIKAVFGTKGFLEDK 237
Db 188 AKSPGTFLLLPDMMIKGLFGKKEFLYQPR 217

Search completed: April 2, 2003, 16:39:32
Job time : 22 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:23:41 ; Search time 17 seconds
(without alignments)
683.650 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MMWLLTTTCLICGTNAGG.....FDFVGLDAPQMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pap.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pap.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pap.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pap.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2137	100.0	395	4	US-09-820-001-2
2	1097	51.3	392	4	US-09-820-001-4
3	1017	47.6	380	1	US-08-227-108-16
4	1017	47.6	380	2	US-09-073-674-16
5	1009	47.2	379	1	US-08-227-108-18
6	1009	47.2	379	2	US-09-073-674-18
7	1004	47.0	379	1	US-08-227-108-3
8	1004	47.0	379	2	US-09-073-674-3
9	1004	47.0	380	1	US-08-227-108-5
10	1004	47.0	380	2	US-09-073-674-5
11	1003	46.9	377	1	US-08-227-108-17
12	1003	46.9	377	2	US-09-073-674-17
13	972	45.5	378	4	US-09-186-489-2
14	118.5	5.5	634	1	US-07-779-049-3
15	118.5	5.5	634	1	US-08-080-240-3
16	100	4.7	932	4	US-09-071-035-416
17	100	4.7	969	4	US-09-071-035-414
18	97	4.5	811	1	US-08-136-743B-4
19	96	4.5	262	2	US-08-602-359A-35
20	95	4.4	559	2	US-09-052-339-1
21	95	4.4	559	4	US-09-385-742B-1
22	95	4.4	767	1	US-08-446-777-8
23	93	4.4	444	2	US-08-485-938A-33
24	90.5	4.2	283	4	US-09-134-001C-5652
25	90.5	4.2	318	4	US-09-134-001C-4156
26	90	4.2	286	4	US-09-355-166-9
27	90	4.2	767	1	US-08-446-777-6

28	89.5	4.2	450	1	US-08-188-582-30	Sequence 30, Appl
29	89.5	4.2	450	1	US-08-646-715-30	Sequence 30, Appl
30	89.5	4.2	494	3	US-08-993-260-3	Sequence 3, Appl
31	89	4.2	297	2	US-08-602-359A-37	Sequence 37, Appl
32	88	4.1	574	2	US-08-756-317-4	Sequence 4, Appl
33	88	4.1	600	2	US-08-756-317-3	Sequence 3, Appl
34	88	4.1	638	2	US-08-756-317-2	Sequence 2, Appl
35	86.5	4.0	441	1	US-08-470-187-8	Sequence 8, Appl
36	86.5	4.0	441	1	US-08-318-905-8	Sequence 8, Appl
37	86.5	4.0	441	1	US-08-483-232-8	Sequence 8, Appl
38	86.5	4.0	441	1	US-08-483-140-8	Sequence 8, Appl
39	86.5	4.0	441	2	US-08-485-938A-8	Sequence 8, Appl
40	86.5	4.0	441	2	US-08-910-041-8	Sequence 8, Appl
41	86.5	4.0	441	3	US-09-328-474-8	Sequence 8, Appl
42	86.5	4.0	441	3	US-09-100-546-8	Sequence 8, Appl
43	86.5	4.0	441	4	US-09-010-715-8	Sequence 8, Appl
44	86.5	4.0	441	4	US-09-577-758-8	Sequence 8, Appl
45	86.5	4.0	835	4	US-09-619-333-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-820-001-2
; Sequence 2, Application US/09820001
; Patent No. 6387680
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE REFERENCE: CLO01186
; CURRENT APPLICATION NUMBER: US/09/820,001
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Human
US-09-820-001-2

Query Match	100.0%	Score	2137;	DB	4;	Length	395;
Best Local Similarity	100.0%	Pred. No.	3.9e-222;				
Matches	395;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MMWLLTTTCLICGTNAGGFLDLENEVPEVMMTSEIIYNGYPSEYEVTTEDGYIL	60				
Db	1	MMWLLTTTCLICGTNAGGFLDLENEVPEVMMTSEIIYNGYPSEYEVTTEDGYIL	60				
Qy	61	LVNRIPIYGRTHARSTGPRPVYMOHALPADNAYWLENANGSLGFLDAGYDVMGNSR	120				
Db	61	LVNRIPIYGRTHARSTGPRPVYMOHALPADNAYWLENANGSLGFLDAGYDVMGNSR	120				
Qy	121	GNTWSRRKTLSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYEIGHSLGTIGF	180				
Db	121	GNTWSRRKTLSETDEKFWAFSDEMAYDLPVDFIVNKTGQEKLYEIGHSLGTIGF	180				
Qy	181	VAFTSMPELAQRIKWNFALGPTISFKYPTGIFTRFPLPNSIIKAVFGTKGFLEDDKTK	240				
Db	181	VAFTSMPELAQRIKWNFALGPTISFKYPTGIFTRFPLPNSIIKAVFGTKGFLEDDKTK	240				
Qy	241	TASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPYSSVHNHILHKLQYH	300				
Db	241	TASTKICNNKILWLICSEFMSLWAGSNKNNQSRMDVYMSHAPYSSVHNHILHKLQYH	300				
Qy	301	SDEFRAYDGNADNNKHYNQSHPIYDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK	360				
Db	301	SDEFRAYDGNADNNKHYNQSHPIYDLTAMKVPTAIWAGGHVLTGTPQDVARILPQIK	360				
Qy	361	SLSLVLSLPEWEPTDFVWGLDAPQMFSGNHL	395				
Db	361	SLSLVLSLPEWEPTDFVWGLDAPQMFSGNHL	395				

Db 361 SLVLVLLPEWPTDFVWGLDAPQRMFSGNHL 395

RESULT 2

US-09-820-001-4
; Sequence 4, Application US/09820001
; Patent No. 6387680
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001186
; CURRENT APPLICATION NUMBER: US/09/820,001
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Human
US-09-820-001-4

Query Match 51.3%; Score 1097; DB 4; Length 392;
Best Local Similarity 53.6%; Pred. No. 7.1e-110;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGLTLAGGLDLENVPEVMNTSEIIYNGYPSEYEYVTTEDGYILL 61
DB 1 MRELGLVCLVLTWLTLSHSGGKLTAVDPETNNVSEIISYWGFPSEYLVETEDGYILL 60
QY 62 VNRIPYGRTHARSTGRPPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 61 LNRIPGRKHNHSDKPKPVVQLHGLLADSSNNVTLNLSLGLFADAGEDVWNGNSRG 120
QY 122 NWSRRHKLSTEDKFAFSDDEMAKYDLPVIDFIVNKTGOEKLYFTGHSIGTTIGV 181
DB 121 NWSRRHKLSTVSQDEFASFDEMAKYDLPASINFILNKTGOEQVYVYVGHSGGTTIGI 180
QY 182 AFTMPPELAQRKMNKALGPTISFKYPTGFTFRFFLLPNSIIKAVGTGKGFLEDKTKI 241
DB 181 AFSQIFELAKRKIMFALGPVAVSACTSPMAKGLRPLDHLIKDLGDKFEFLPQSAFLAW 240
QY 242 ASTKICNNKILMICSEFSLWAGSNKKNQSMQMDVYMSHAPTGSVNHILHIKOLYHS 301
DB 241 LGPHVCTHVLKELCGLNLCFLCGLGFEERNLNRSVDVYTHSPAGTSVQNMHLWSQAVF 300
QY 302 DEFRAYDNGNDNMKNHNSHPPIYDLTAMKVPTAIWAGGHDLGTPQDVARILPOIKS 361
DB 301 QKFOAFDMSSAKNYHYNQSPPTTNNKMLVPTAVWSGGHDLADYDVNILLTQITN 360
QY 362 LSLVLVLLPEWPTDFVWGLDAPQRMFSGNHL 395
DB 361 LVPHES-IPWE-HLDFINGLDAPWLYNKIINL 392

RESULT 3

US-08-227-108-16
; Sequence 16, Application US/08227108
; Patent No. 5807726
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,108
; FILING DATE: 03-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A. 256
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 7620-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-108-16

Query Match 47.6%; Score 1017; DB 1; Length 380;

Best Local Similarity 50.3%; Pred. No. 2.9e-101;

Matches 190; Conservative 68; Mismatches 108; Indels 12; Gaps 4;
QY 14 GTNLAGGLDLENVPEVMNTSEIIYNGYPSEYEYVTTEDGYILLVNRIPYGRTHAR 73
DB 3 GKLHFG-----SPEVTMNIISOMITWYGPNEEYEVTTEDGYILEVNRIPYCKKNSG 53
QY 74 STGRPPVYVMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRGNTWRRHKLSE 133
DB 54 NTGQRVFLQLHGLASATNINLPNLSLAFILADAGYDVWNGNSRGNTWRRNLYSP 113
QY 134 TDEKFW-AFSFDEMAKYDLPVIDFIVNKTGOEKLYFTGHSIGTTIGVAFSTMPPELAOR 192
DB 114 DSVEFWAASFDEMAKYDLPATIDFIVKTKGQQLHYVGHSGGTTIGTAFSTNPSLAKR 173
QY 193 IKMNFALGPTISFKYPTGFTFRFFLLPNSIIKAVGTGKGFLEDKTKIATSKICNNKTL 252
DB 174 IRTFALAPAVATVYTKSLINKLRFPVQSLFPIEDKIFYPHNPFDQFLATEVCSREML 233
QY 253 WLICSEFSLWAGSNKKNQSMQMDVYMSHAPTGSVNHILHIKOLYHSDEFRAYDWGND 312
DB 234 NLLCSNALFICGFSKNTSRLDVLVLSHPAGTSVQNMFWHTQAVKSGKQAYDWGSP 293
QY 313 ADMKNHNSHPPIYDLTAMKVPTAIWAGGHDLGTPQDVARILPOIKSLSLVLSLLPEW 372
DB 294 VQNRMHYDQSPYXNVNTAMNVPVIAVWNGKDLLADPQDVGLLLPKLPNL-IYHKBIPIY 352
QY 373 EPTDFVWGLDAPQRMFS 390
DB 353 N-HLDFIWDAPQEVIN 369

RESULT 4

US-09-073-674-16
; Sequence 16, Application US/09073674
; Patent No. 5998189
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor

STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-674-16

Query Match 47.6%; Score 1017; DB 2; Length 380;
Best Local Similarity 50.3%; Pred. No. 2.9e-101;
Matches 190; Conservative 68; Mismatches 108; Indels 12; Gaps 4;
Qy 14 GTLNAGGFLDLENEVNPVMTSTIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHAR 73
Db 3 KGLHPG-----SPEVTNISOITWYGPNEEYEVTTEDGYILEVNRIPYGRTHAR 53
Qy 74 STGPRVYVYMHQALFADNAYWLENGSLGFLADAGYVWNGSRGTWRRHKTLSL 133
Db 54 NTGQRPVVLQHLGLASATNLSNLPNNLSAFILADAGYVWNGSRGTWARRNLYSP 113
Qy 134 TDEKFW-AFSEDEMAKYDLPVIDFIVNKTQEKLYFGHSLGTTIGVAFSTMPDLAQR 192
Db 114 DSVEFWAAFSDEMAKYDLPVIDFIVNKTQEKLYFGHSLGTTIGVAFSTMPDLAQR 173
Qy 193 IKMNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFLEDKTKIASTKICNNKIL 252
Db 174 IKTYALAPVATVYTKSLINKLRFVPSQSLFKIFGDKIFYPHNFDDQFLATEVCSREML 233
Qy 253 WLICSEFMSLWAGSNKKNQSDVYVMSHAPTGSVVHNLHIKQLYHSDEFRAVDWGNQ 312
Db 234 NLLCSNALFIICGDSKNFNTSRDLVYLSHNPAGTSVQNMFHWTQAVKSGKFAQYDWGSP 293
Qy 313 ADNMKHYNQSPHYDITAMKVPITAWAGGHVDVLTGTPDVARILPOIKSLSLVSLLEPW 372
Db 294 VONRMHYDQSPHYDITAMKVPITAWAGGHVDVLTGTPDVARILPOIKSLSLVSLLEPW 352
Qy 373 EPTDEVNGLDAPORMFS 390
Db 353 N-HLDFIWMADAPQEVYN 369

RESULT 5
US-08-227-108-18
Sequence 18, Application US/08227108
Patent No. 5807726
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Panucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-227-108-18

Query Match 47.2%; Score 1009; DB 1; Length 379;
Best Local Similarity 51.1%; Pred. No. 2.1e-100;
Matches 185; Conservative 69; Mismatches 106; Indels 2; Gaps 1;
Qy 29 NPEVMTSTIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHARSTGPRVYVYMHQALF 88
Db 9 NPEVMTSTIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHARSTGPRVYVYMHQALF 68
Qy 89 ADNAYWLENGSLGFLADAGYVWNGSRGTWRRHKTLSLSEDEMAK 148
Db 69 ASASWISNLPNNLSAFILADAGYVWNGSRGTWRRHKTLSLSEDEMAK 128
Qy 149 YDLPVIDFIVNKTQEKLYFGHSLGTTIGVAFSTMPDLAQRIMKFAFGPTISFKY 208
Db 129 YDLPVIDFIVNKTQEKLYFGHSLGTTIGVAFSTMPDLAQRIMKFAFGPTISFKY 188
Qy 209 TGIFTRFLLPNSIIKAVFGTKGFLEDKTKIASTKICNNKILWLICSEFMSLWAGSNK 268
Db 189 KSLVNLKRFIPPTWFKIFGDKIFYPHNFDDQFLATEVCSRETLNVICSNALFIICGDS 248
Qy 269 KMNQSRMDVYVMSHAPTGSVVHNLHIKQLYHSDEFRAVDWGNQADNMKHYNQSPHY 328
Db 249 ANLMSRLDVSVHNPAGTSVQNMFHWTQAVKSGKFAQYDWGSP 308
Qy 329 LTAMKVPITAWAGGHVDVLTGTPDVARILPOIKSLSLVSLLEPWETDFVYVGLDAPORM 388
Db 309 VTAMNPIAVWNGSGNDLADQDQVDDLLLPKLSNLIYHKEILP--YHNLDFIWMADAPQEV 366
Qy 389 FS 390
Db 367 YN 368

RESULT 6
US-09-073-674-18
Sequence 18, Application US/09073674
Patent No. 5998189
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis


```

; Patent No. 5998189
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,674
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crissey, Todd M.
; REGISTRATION NUMBER: 37,807
; REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 734 622-7530
; TELEFAX: 734 622-1553
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-674-3

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Query Match 47.0%; Score 1004; DB 2; Length 379;
Best Local Similarity 50.3%; Pred. No. 7.3e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMTSEIIYNGYSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHALF 88
Db 9 NPEVTMISQITWGYPAEYEVVTDGYILGIDRIPYGRKNSNIGRRPVAFLOHGLL 68

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSDETDEKFWAFSDEMAK 148
Db 69 ASATNWSLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSDEMAK 128

Qy 149 YDLPGVIDFVYKNGOEKLYFIGHSLGTTIGFAVFTSTPELAQRKMNFGALGPTISFKYP 208
Db 129 YDLPATIDFILKKTGQDKLHVHSGQTTIGFIAPSTNPKLAKRIKTFYALAPVATVKYT 188

Qy 209 TGIETREFLLNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLICSEFMSLWAGSNK 268
Db 189 ETLLNKLMLVPSFLKIFGNKIYPPHFFDQFLATEVCSRETVDLCSNALFIICGPD 248

Qy 269 KMNQSRMDVYMSHAPTGSSVHNILHKLHYSDEFRAYDNGNDADNNKHVNSHPPIYD 328
Db 249 MNLNMSRLDVLVLSNPACTSVQNVLHWSQAVKSGKQFADWGSVPQNMHHYHQSPPYYN 308

Qy 329 LTAMKVPTAIWAGGHVLTGTPQDVARILPQIKSLVLSLLPEWEPTDFVWGLDAPQRM 388
Db 309 LTDHVPITAVWNGNDLLADPHDVLDSLLKLPNL-IYHRKIPPNY-HLDFIWMADPOAV 366

Qy 389 FS 390
Db 367 YN 368

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RESULT 9

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US-08-227-108-5
; Sequence 5, Application US/08227108
; Patent No. 5807726
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benicourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,108
; FILING DATE: 03-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 7620-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-108-5

```

```

Query Match 47.0%; Score 1004; DB 1; Length 380;
Best Local Similarity 50.3%; Pred. No. 7.4e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMTSEIIYNGYSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVYMQHALF 88
Db 10 NPEVTMISQITWGYPAEYEVVTDGYILGIDRIPYGRKNSNIGRRPVAFLOHGLL 69

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSDETDEKFWAFSDEMAK 148
Db 70 ASATNWSLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSDEMAK 129

Qy 149 YDLPGVIDFVYKNGOEKLYFIGHSLGTTIGFAVFTSTPELAQRKMNFGALGPTISFKYP 208
Db 130 YDLPATIDFILKKTGQDKLHVHSGQTTIGFIAPSTNPKLAKRIKTFYALAPVATVKYT 189

Qy 209 TGIETREFLLNSIIKAVFGTKGFLEDDKTKIASTKCNKILWLICSEFMSLWAGSNK 268
Db 190 ETLLNKLMLVPSFLKIFGNKIYPPHFFDQFLATEVCSRETVDLCSNALFIICGPD 249

Qy 269 KMNQSRMDVYMSHAPTGSSVHNILHKLHYSDEFRAYDNGNDADNNKHVNSHPPIYD 328
Db 250 MNLNMSRLDVLVLSNPACTSVQNVLHWSQAVKSGKQFADWGSVPQNMHHYHQSPPYYN 309

Qy 329 LTAMKVPTAIWAGGHVLTGTPQDVARILPQIKSLVLSLLPEWEPTDFVWGLDAPQRM 388
Db 310 LTDHVPITAVWNGNDLLADPHDVLDSLLKLPNL-IYHRKIPPNY-HLDFIWMADPOAV 367

Qy 389 FS 390
Db 368 YN 369

```

RESULT 10

US-09-073-674-5
; Sequence 5, Application US/09073674
; Patent No. 598189
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benichourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Road
; CITY: Ann Arbor
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,674
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crissey, Todd M.
; REGISTRATION NUMBER: 37,807
; REFERENCE/DOCKET NUMBER: 5072-D1-66-TWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 734 622-7530
; TELEFAX: 734 622-1553
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-674-5

Query Match 47.0%; Score 1004; DB 2; Length 380;
Best Local Similarity 50.3%; Pred. No. 7.4e-100;
Matches 182; Conservative 70; Mismatches 108; Indels 2; Gaps 2;

Qy 29 NPEVMMNTSEIIYNGYSEEEYVETEDGYILLVNRIPYGRTHARSTGPRPVVYMHQHALF 88
Db 10 NPEVTMISQMTYGYPAEEYEVVETEDGYILGIDRIPYGRKNSENIGRRPVAFLOHGLL 69

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFWAFSDEMAK 148
Db 70 ASATNWSNLNPNLSLAFILADAGYDVWLGNSRGNTWARRNLYSPDSVEFWAFSDEMAK 129

Qy 149 YDLPGVIDFVNTGOEKLFTGSLGTTIGFVAFSTPELAQRKIMFALGPTISFKYP 208
Db 130 YDLPATIDFLKKTQDKLHYVGHSGQTIGFIAFSTNPKLAKRIKTFYALAPVATVKT 189

Qy 209 TGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKIASTKICNNKILWLICSEFMSLWAGSNK 268
Db 190 ETLNKLMLVPSFLKFLFNGKIFYPHFHFDQFLATEVCSRTVDLLCSNALFIICGDT 249

Qy 269 KNNQSRMDVYMSHAPTSSVHNILHIKQLYHSDFRAYDNGNDADNMKHYNQSHPPYD 328
Db 250 MNLNLSRLDVLVLSHPAGTSVQVNLHWSQVKSQKGFQAFDWSGVQNNMHHYHQSPPYYN 309

Qy 329 LFAMKVPYTAIWAGGHVLTGPDDVARILPQIKSLSLVLSLPEWEPTDFVWGLDAPQRM 388
Db 310 LTDHVPYIAVWNGNDLLADPHDVLKLPNL-IYHRKIPPNY-HLDFIWMADPAQAV 367

Qy 389 FS 390
::

Db 368 YN 369

RESULT 11

US-08-227-108-17
; Sequence 17, Application US/08227108
; Patent No. 5807726
; GENERAL INFORMATION:
; APPLICANT: Blanchard, Claire
; APPLICANT: Benichourt, Claude
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: Recombinant Dog Gastric Lipase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,108
; FILING DATE: 03-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Panucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 7620-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-227-108-17

Query Match 46.9%; Score 1003; DB 1; Length 377;
Best Local Similarity 50.6%; Pred. No. 9.3e-100;
Matches 183; Conservative 64; Mismatches 113; Indels 2; Gaps 1;

Qy 29 NPEVMMNTSEIIYNGYSEEEYVETEDGYILLVNRIPYGRTHARSTGPRPVVYMHQHALF 88
Db 9 NPEANMISQMTYGYPCQEEYEVVETEDGYILGVYRIPHGKNNSENIGKRPVYVYLQHGLI 68

Qy 89 ADNAYWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSLTDKFWAFSDEMAK 148
Db 69 ASATNWSNLNPNLSLAFILADAGYDVWLGNSRGNTWSRKNYVSPDSVEFWAFSDEMAK 128

Qy 149 YDLPGVIDFVNTGOEKLFTGSLGTTIGFVAFSTPELAQRKIMFALGPTISFKYP 208
Db 129 YDLPATINFIYVQKGOEKIHYVGHSGQTIGFIAFSTNPKLAKRIKTFYALAPVATVKT 188

Qy 209 TGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKIASTKICNNKILWLICSEFMSLWAGSNK 268
Db 189 QSLPKKISIFITFLFKLMFGKKMFLPHYFDLGTVECSREVLDDLLCSNTLFIICGFDK 248

Qy 269 KNNQSRMDVYMSHAPTSSVHNILHIKQLYHSDFRAYDNGNDADNMKHYNQSHPPYD 328
Db 249 KNLNYSRFDVYLGHNPACTSVQDFLHWAQLVRSKGFQAFNNGSPSQNNMLHYNQKTPPEYD 308

Qy 329 LFAMKVPYTAIWAGGHVLTGPDDVARILPQIKSLSLVLSLPEWEPTDFVWGLDAPQRM 388
Db 309 VSAMTPVAVWNGNDLLADPDQVAMLLPKLSNLLFHKLEILA--YNHLDIFIWMADPAQEV 366


```

; APPLICANT: IWAMI, MORITA
; APPLICANT: KOJO, HITOSHI
; TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/779,049
; FILING DATE: 19911018
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5310659man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-723-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-779-049-3

```

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Query Match 5.5%; Score 118.5; DB 1; Length 634;
Best Local Similarity 20.3%; Pred. No. 0.00064;
Matches 92; Conservative 55; Mismatches 138; Indels 169; Gaps 23;

```

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QY 5 LLTTCCLIGTLAGGFLDLENEVPVW---MNTSEII-----IYNGYPSSEY 50
DB 10 MLLTVLVTSLSVAFGSGEQEAEELQYELKTDVMVEMRDGVKLPDIIY--LPVAKT 67
QY 51 EVTTEDGYILLNRPYGR--THARSTGPRPVYMQHALFADNAYWLENYANGSLGFLAD 109
DB 68 EQEKKDGFPTLVFRTYPYKDTYKTEGP-----FFAK 99
QY 110 AGYDVMGNSRGNTWSRRHKTLSDEKFWAFSFDMAK--YDL---PGVIDFVNTKQ 164
DB 100 RGVAVVVDTRG-----RYKSEGE-----WNFVDD-AKGDYDLIEWAAVQDFSTGKVG 148
QY 165 EKLFIHSLGTTIGFVAFSTPELAQRKIMNFALGPTISFKYPTGIFTRFLLPNSIIK 224
DB 149 MGLSYMAY---TQYVLAESKPPHLVTMIPLEGMSNPA-----E 183
QY 225 AVFGTKGFFLEDKTKIASTKICNNKILWICSEFMSLWAG-----SNKKNMQ 273
DB 184 EVFETGGAMQLDR-----YLSWTLGQAVDTFARRLDEKNGNTVQ 222
QY 324 PPIYDLTAMKVPPTAIWAGHDVL--GTPOD-----VARTLPQISLSVLVS---L 368
DB 271 SPOEQHDTPVPYHYVGGWYDILLNGTSKNYIGITENGPTERYLPALAKTVNIQDTQKLL 330
QY 369 LPWE-----PTPDFVWGLDAPQMFSGNHN 394
DB 331 IGPWTHGYQTAVGTFNE-----PKADLSDVHN 358

```

```

RESULT 15
US-08-080-240-3
; Sequence 3, Application US/08080240
; Patent No. 5312750
; GENERAL INFORMATION:
; APPLICANT: ARAMORI, ICHIRO
; APPLICANT: FUKAGAWA, MASAO
; APPLICANT: ONO, HIROKI
; APPLICANT: ISHITANI, YOSUKE
; APPLICANT: TSUMURA, MANA
; APPLICANT: IWAMI, MORITA
; APPLICANT: KOJO, HITOSHI
; TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/080,240
; FILING DATE: 19930622
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5312750man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-803-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-080-240-3

```

```

Query Match 5.5%; Score 118.5; DB 1; Length 634;
Best Local Similarity 20.3%; Pred. No. 0.00064;
Matches 92; Conservative 55; Mismatches 138; Indels 169; Gaps 23;
QY 5 LLTTCCLIGTLAGGFLDLENEVPVW---MNTSEII-----IYNGYPSSEY 50
DB 10 MLLTVLVTSLSVAFGSGEQEAEELQYELKTDVMVEMRDGVKLPDIIY--LPVAKT 67
QY 51 EVTTEDGYILLNRPYGR--THARSTGPRPVYMQHALFADNAYWLENYANGSLGFLAD 109
DB 68 EQEKKDGFPTLVFRTYPYKDTYKTEGP-----FFAK 99
QY 110 AGYDVMGNSRGNTWSRRHKTLSDEKFWAFSFDMAK--YDL---PGVIDFVNTKQ 164
DB 100 RGVAVVVDTRG-----RYKSEGE-----WNFVDD-AKGDYDLIEWAAVQDFSTGKVG 148
QY 165 EKLFIHSLGTTIGFVAFSTPELAQRKIMNFALGPTISFKYPTGIFTRFLLPNSIIK 224
DB 149 MGLSYMAY---TQYVLAESKPPHLVTMIPLEGMSNPA-----E 183
QY 225 AVFGTKGFFLEDKTKIASTKICNNKILWICSEFMSLWAG-----SNKKNMQ 273
DB 184 EVFETGGAMQLDR-----YLSWTLGQAVDTFARRLDEKNGNTVQ 222
QY 274 SRM-----DVMSHAPGTGSSVHNILTKOLYHSDFRAYDWGNDADNNKHYNQ---SH 323
DB 223 DKIKKALDDYERKWLHNMPRS-----KVAPLQNM-----IDWKEAMDPHEDEYWKSI 270

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Qy 324 PFIYDLTAMKVPTAIWAGHDVL--GTPQD-----VARILPQIKSLSLVLS-----L 368
| | | | | : | | : | | : |
Db 271 SPQEQHDTWPVPTYHHVGGWDILLNGTSKNYIGITENGPTERYLPALKTYVNIQDTQKLL 330
Qy 369 LPENE-----PTFDFVWGLDAPQRMFSGNHN 394
| | | | | : | | : | | : |
Db 331 IGPWTHGYPQTAVGTENF-----PKADLSDVHN 358

Search completed: April 2, 2003, 16:35:25
Job time : 19 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2003, 16:39:24 ; Search time 46 seconds
(without alignments)
825.502 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MWLLTTTCLICGTLAGG.....FDFVWGLDAPQRMFSGNHL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1099	51.4	399	2 G01416	lysosomal acid lip
2	1097	51.3	399	2 S41408	lysosomal acid lip
3	1052	49.2	398	2 S07145	triacylglycerol li
4	1022.5	47.8	395	1 L1RTP	triacylglycerol li
5	982.5	46.0	397	1 JC4017	triacylglycerol li
6	663.5	31.0	405	2 T22675	hypothetical prote
7	644.5	30.2	403	2 T33198	hypothetical prote
8	634	29.7	411	2 T22290	hypothetical prote
9	613	28.7	405	2 H88930	protein R11G11.14
10	585.5	27.4	411	2 G89074	protein R04A8.5 [1
11	546.5	25.6	426	2 T20480	hypothetical prote
12	502.5	23.5	559	2 J70949	egg-specific prote
13	469.5	22.0	1585	2 T31611	hypothetical prote
14	436	20.4	443	2 T39540	triglyceride lipas
15	405	19.0	467	2 T41053	triglyceride lipas
16	402.5	18.8	344	2 E84526	probable lysosomal
17	347.5	16.3	413	2 T43170	probable triacylg
18	342.5	16.0	548	2 S37969	probable triacylg
19	320	15.0	460	2 T39443	probable triglycer
20	293	13.7	431	2 D86318	protein F15H18.6 [
21	224	10.5	509	2 G96766	protein lipase F2P
22	219.5	10.3	573	2 S64754	probable membrane
23	209	9.8	538	2 S64842	probable membrane
24	147	6.9	336	2 F83425	probable esterase/
25	120	5.6	40	2 I19539	triacylglycerol li
26	118.5	5.5	634	2 I40217	glutaryl 7-ACA acy
27	118	5.5	456	2 E69391	hypothetical prote
28	115	5.4	62	2 S59904	lipase, pregastric
29	111	5.2	297	2 T21632	hypothetical prote

30 111 5.2 300 2 C69664 carboxylesterase N
31 108.5 5.1 300 2 I40425 carboxylesterase (platelet-activatin
32 103.5 4.8 436 2 JC5021 Sd protein - fruit
33 102.5 4.8 363 2 S18765 lipoprotein [impor
34 101.5 4.7 789 2 G30587 laccase (EC 1.10.3
35 101 4.7 573 2 T02743 hypothetical prote
36 100.5 4.7 371 2 T24853 tributyrin esteras
37 100 4.7 259 2 E95071 tributylin esteras
38 100 4.7 259 2 C97939 tributylin esteras
39 99.5 4.7 185 2 F69767 hypothetical prote
40 99.5 4.7 329 2 D97340 DNA replication pr
41 99.5 4.7 330 2 A10084 thiamin-binding pe
42 99 4.6 804 2 B48687 ribonucleoside-dip
43 98 4.6 286 2 D75217 probable 2-acetyl-
44 98 4.6 1155 2 H71456 probable pyrolysin
45 97.5 4.6 304 2 A89905 hypothetical prote

ALIGNMENTS

RESULT 1

G01416

lysosomal acid lipase - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999

C:Accession: G01416

R:Du, H.

submitted to the EMBL Data Library, April 1994

A:Reference number: G06919

A:Accession: G01416

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-399 <DUX>

A:Cross-references: EMBL:U08464; NID:G505052; PIDN:AAB60328.1; PID:G505053

C:Superfamily: triacylglycerol lipase, lingual

C:Keywords: glycoprotein

Query Match 51.4%; Score 1099; DB 2; Length 399;
Best Local Similarity 53.6%; Pred. No. 2.3e-85;
Matches: 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGTLAGGFLDLENEVPEVMMNTSEIIYNGYPSSEYEVETEDGYILL 61
Db 3 MRFLGVVCLVLTLSHSGRGKLTAVDPETNMNVSEIISYWGFPSEYLVETEDGYILL 62
Qy 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
Db 63 LNRIPHGKRNHSDKGPKEPVFLQHGGLADSSNMWVTNLANSLSGFLADAGYDVMGNSRG 122
Qy 122 NTWSRRHKTSETDEKFWAFSDEMAYDLPQVIDFVNGTGOEKLIFIGHSLGTTIGFV 181
Db 123 NTWSRKHKTLSVQDEFWAFSDEMAYDLPASINFLINKTGOEQVYVGHSGQTIGFI 182
Qy 182 AFTSMPELAQRKMFALGPTISFKYPTGIFTRFELPNSIIKAVFGTKGFEDDKTKI 241
Db 183 AFSQIPELAKRIKFFALGPVAVAFCTSPNAKLGRLPDHLIKLDFGDKFEPQSAFLKW 242
Qy 242 ASTKICNNKIWLICSEFNSLWAGSNKKMNQSDMVTMSHAPTSGSSVHNLIHKQLVHS 301
Db 243 LGTHVCTHVLKELCGNLCLFLLCGFNERNLNMSRDVYTTTHSPAGTSVQNMLHWSQAVKF 302
Qy 302 DEFAYDKNDADNKKHYNQSHPIYDLTAMKVPTAIWAGDDVLGTQDQVARILPOLKS 361
Db 303 QKQAFDMGSSAKNYFHYNQSPPTYNVKMDLVPVAVWSGGHDLADYVDVNNILLTQITN 362
Qy 362 LSLVLSLPEWEPTDFVWGLDAPQRMFSGNHL 395
Db 363 LVFHES-IPENE-HLDFIWLGLDAPWRLYNKLIINL 394

RESULT 2

S41408

lysosomal acid lipase (EC 3.1.1.-) / sterol esterase (EC 3.1.1.13) precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S41408; A39315; S47187
R:Amels, D.; Merkel, M.; Eckerstorn, C.; Greten, H.
Eur. J. Biochem. 219, 905-914, 1994
A:Title: Purification, characterization and molecular cloning of human hepatic lysosomal
A:Reference number: S41408; MUID:94155897; PMID:8112342
A:Accession: S41408
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-399 <AME>
A:Cross-references: EMBL:X76488; NID:g434305; PIDN:CAA54026.1; PID:g434306
R:Anderson, R.A.; Sando, G.N.
J. Biol. Chem. 266, 22479-22484, 1991
A:Title: Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl
A:Reference number: A39315; MUID:92042192; PMID:1718995
A:Accession: A39315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'P', 17-399 <AND>
A:Cross-references: GB:M74775; NID:g187151; PIDN:AAA59519.1; PID:g187152
R:Du, H.; Gregory, G.A.
Submitted to the EMBL Data Library, April 1994
A:Description: Structural conservation of putative functional motifs between mouse and h
A:Reference number: S47187
A:Accession: S47187
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-22, 'R', 24-399 <DUH>
A:Cross-references: EMBL:D31690; NID:g506430; PIDN:CAA83495.1; PID:g506431
C:Genetics:
A:Gene: GDB:LIPA
A:Cross-references: GDB:120153; OMIM:278000
A:Map position: 10q24-10q25
C:Superfamily: triacylglycerol lipase, lingual
C:Keywords: carboxylic ester hydrolase; glycoprotein

Query Match 51.3%; Score 1097; DB 2; Length 399;
Best Local Similarity 53.6%; Pred. No. 3.4e-85;
Matches 211; Conservative 63; Mismatches 118; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGFLDENEVPMVNTSEIIYNGYPSSEEVETEDGYILL 61
DB 3 MRFGLDVCLVLTLSHSGSGKLTAVDPETNNVSEIISYWGFPSEYLVETEDGYILL 62
QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENANGSLGFLADAGYDVWNGNSRG 121
DB 63 LNRIPGRKHNHSDKGPVFLQHGLLADSSNWNVLANSLSGFLADAGYDVWNGNSRG 122
QY 122 NTSRRHKTLSSETDEKFAFSEDEMAKYDLPGVDFIVNKTGOEKLIFYGHSLGTTIGFV 181
DB 123 NTSRRHKTLSVSQDEFAFSEDEMAKYDLPASINFILNKTGOEQVYVYVGHSGQTTIGF 182
QY 182 AFTMPQLAQRKIMFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKI 241
DB 183 AFSQIPELAKRIMFALGPVAVSFCTSPMAKGLRDLPHLLKDLFGDKEFLPQSAFLKW 242
QY 242 ASTKICNNKILICSEFMSLWAGSNKMNOSRMDVYMSHAPTSSSVNIIHLHIKOLYHS 301
DB 243 LGTHVCTHVLKELGCLNCLFLLCGNERNLANSRDVYTHSPAGTSVQNMHLHWSQAVKF 302
QY 302 DEFRAVDGNDADNNKHYNQSHPPYIDLTAMKVPTAINAGGHVLTGTPQDVARIILPOIKS 361
DB 303 QKQFAFDGSSAKNYFHYNQSPYPTYNVNDMLVPTAVWGGHDLADYVDVNNILLTQTIN 362
QY 362 LSLVLSLLPEWEPTDFVWGLDAPORMSGNNL 395
DB 363 LVFHES-IPWE-HLDFINGLDAPRLYNKIINL 394

RESULT 3
S07145

triacylglycerol lipase (EC 3.1.1.3) precursor, gastric - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1999
C:Accession: S07145; S27102; S04942
R:Boomer, M.W.; Angal, S.; Farranton, G.T.; Harris, T.J.R.; Lyons, A.; King, D.J.; Pi
Biochim. Biophys. Acta 909, 237-244, 1987
A:Title: Molecular cloning of a human gastric lipase and expression of the enzyme in
A:Reference number: S07145; MUID:87299724; PMID:3304425
A:Accession: S07145
A:Molecule type: mRNA
A:Residues: 1-398 <BOD1>
A:Cross-references: EMBL:X05997; NID:g31771; PIDN:CAA29413.1; PID:g758063
A:Accession: S27102
A:Molecule type: protein
A:Residues: 20-24, 'X', 26, 'X', 28-33, 'X', 35-42, 'X', 44, 'X', 46-48, 'X', 50, 'X', 52, 'X', 54-56
A:Note: it is uncertain whether Met-1 or Met-7 is the Initiator
R:Bernbeck, S.; Blaackberg, L.
Eur. J. Biochem. 182, 495-499, 1989
A:Title: Human gastric lipase. The N-terminal tetrapeptide is essential for lipid bin
A:Reference number: S04942; MUID:89325292; PMID:2753032
A:Accession: S04942
A:Molecule type: protein
A:Residues: 20-45 <BER>
C:Superfamily: triacylglycerol lipase, lingual
C:Keywords: carboxylic ester hydrolase; extracellular protein; glycoprotein; lipid di
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-398/Product: triacylglycerol lipase, gastric #status experimental <MAT>
F:34,99,185,271/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.2%; Score 1052; DB 2; Length 398;
Best Local Similarity 50.4%; Pred. No. 2.2e-81;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGFLDENEVPMVNTSEIIYNGYPSSEEVETEDGYILL 61
DB 1 MWLLTMAISLVLTGTLGFLGKLPSPGSEVPMNISMITYWGYNEEVETEDGYILLE 60
QY 62 VNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENANGSLGFLADAGYDVWNGNSRG 121
DB 61 VNRIPYKNGKSGTQRPVFLQHGLLASATNWNLSLNNPNSLAFLADAGYDVWNGNSRG 120
QY 122 NTSRRHKTLSSETDEKFAFSEDEMAKYDLPGVDFIVNKTGOEKLIFYGHSLGTTIGFV 181
DB 121 NTSRRHKTLSVSQDEFAFSEDEMAKYDLPATIDFIVKTKGQKQLHYVGHSGQTTIGF 180
QY 182 AFTMPQLAQRKIMFALGPTISFKYPTGIFTRFFLLPNSIIKAVFGTKGFFLEDKTKI 241
DB 181 AFTNPQLAKRITKTYALAPVATVYTKSLINKLRFVPSLKFIFGDKIFYPHNFDDQF 240
QY 242 ASTKICNNKILICSEFMSLWAGSNKMNOSRMDVYMSHAPTSSSVNIIHLHIKOLYHS 301
DB 241 LATEVCSREMLNCLGSLNALFIICGFDKSNFNTSRDLVYLSHNPAGTSVQNMHFWHTQAVKS 300
QY 302 DEFRAVDGNDADNNKHYNQSHPPYIDLTAMKVPTAINAGGHVLTGTPQDVARIILPOIKS 361
DB 301 GRQYDWDGSPVONRMHDDQSPPIYNTAMNVPVIAVWNGKDLLADPDQVGLLLPKLPN 360
QY 362 LSLVLSLLPEWEPTDFVWGLDAPORMFS 390
DB 361 L-IYHKEIPFYN-HLDFIWMADAPQEVYN 387

RESULT 4
LIRTT
triacylglycerol lipase (EC 3.1.1.3) precursor, lingual - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 11-Jun-1999
C:Accession: A23045
R:Doeherty, A.J.P.; Bodmer, M.W.; Angal, S.; Verger, R.; Riviere, C.; Lowe, P.A.; Lyo
Nucleic Acids Res. 13, 1891-1903, 1985
A:Title: Molecular cloning and nucleotide sequence of rat lingual lipase cDNA.
A:Reference number: A23045; MUID:85215587; PMID:3839077
A:Accession: A23045

```

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-39/Product: pregastric esterase #status predicted <MAT>
F:33,70,326/Binding site: carboxylate (Asn) (covalent) #status predicted
F:171/Active site: Ser #status predicted

Query Match          46.0%; Score 982.5; DB 1; Length 397;
Best Local Similarity 47.3%; Pred. No. 1.8e-75;
Matches 184; Conservative 72; Mismatches 130; Indels 3; Gaps

Qy 2 MWLLLTTCICGTLNAGGFLDLENEVNPVWMTSEIIYNGYPSEEVETTEDGYILL 61
Db 1 MWLLLVTVCFTHMSGNAFCFLG-KIAKNPEASNVSMISYGCYPSMHKVIADGYILQ 59

Qy 62 VNRIPYGRTHARSTGPRPVYMQHALPADNAYWLENVANGSLGFLADAGYDVWNGSRG 121
Db 60 VYRPHGKNANHLGQRPPVYFLOHGLGSGATWISNLPKNSLGFLLADAGYDVWLGNSRG 119

Qy 122 NTWSSRRKTLSETDEKFWASFDEMAKYDLPGVITDFIVNKTGQEKLYFIGHSLGTTIGFV 181
Db 120 NTAQEHLYYSPDSPEFAWSEFDEMAKYDLPSPIDFILRTGQKKLHYVGHSGCTIGFI 179

Qy 182 AFSMPELAQRKMNFAALGTISFKYPTGIFTFRFFLLPNSIIKAVFTGKGFLEDDKTKI 241
Db 180 AFSSTPLAEKIKVFYALAPVATVKYTKSLFNKLALIPHLFKIIFGDKMFPHTLEQF 239

Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNQSRMDVYNSHAPTGSVHNLIHIKOLYHS 301
Db 240 LGVEMCSRETLDVLCKNALFAITGVDNKNFMSRLDYVIAHNPAQTSVQNTLHWROAVKS 299

Qy 302 DEFRAWDGNDADNMKNYNSHPPIYDLTAMKYPTATWAGGHVDVLGTPODVARILPQIKS 361
Db 300 GKFOAFQWGPYQNLHYHOPTPIYLLTAMNYPVIAWSADNLLADPOVDVDFLLSKLSN 359

Qy 362 LSLVLSLLPEWEPTEFVWGLDAPORMFS 390
Db 360 L-IYHKEIPNYN-HLDFIWDADAPQEVYN 386

RESULT 6
T22675
hypothetical protein F5AF3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T22675
R:Percy, C.; Lloyd, C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19598
A:Accession: T22675
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-405 <WIL>
A:Cross-references: EMBL:Z79696; PIDN:CAB01973.1; GSPDB:GN00023; CESP:F5AF3.3
A:Experimental source: clone F54F3
C:Genetics:
A:Gene: CESP:F54F3.3
A:Map position: 5
A:Introns: 31/3; 65/1; 274/3; 366/3
C:Superfamily: triacylglycerol lipase, lingual

Query Match          31.0%; Score 663.5; DB 2; Length 405;
Best Local Similarity 37.8%; Pred. No. 2.1e-48;
Matches 151; Conservative 68; Mismatches 154; Indels 27; Gaps

Qy 1 MWLLLTTCICGTLNAGGFLDLENEVNPVWMTSEIIYNGYPSEEVETTEDGYIL 60
Db 7 VMLAVLATAATVFG-----HDADPEMKMTTQIIIMRWGYPAMIIDVTEDGYIL 55

Qy 61 LVNRIPIYGRTHAR-STGPRPVYMQHALPADNAYWLENVANGSLGFLADAGYDVWNGSN 119
Db 56 ELHRIPIYGRKNTVWPNGKKPVVFMQHCLECSSSNVWVNLPTESAFILFADAGYDVWLGNF 115

Qy 120 RGNTWSRRHKTGETDEKFWASFDEMAKYDLPGVITDFIVNKTGQEKLYFIGHSLGTTIG 179
Db 120 NTAQEHLYYSPDSPEFAWSEFDEMAKYDLPSPIDFILRTGQKKLHYVGHSGCTIGFI 179

```


RESULT 12

JT0949

egg-specific protein - silkworm

C:Species: Bombyx mori (silkworm)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 26-Feb-1998

C:Accession: JT0949; A28527

R:Sato, Y.; Yamashita, O.

submitted to JIPID, September 1991

A:Reference number: JT0949

A:Accession: JT0949

A:Molecule type: DNA

A:Residues: 1-559 <SAT>

A:Experimental source: larva

A:Note: this protein is a homotrimer

R:Indraaith, L.S.; Sasaki, T.; Yamashita, O.

J. Biol. Chem. 263, 1045-1051, 1988

A:Title: A unique protease responsible for selective degradation of a yolk protein in Bc

A:Reference number: A28527; MUID:88087166; PMID:3275655

A:Accession: A28527

A:Molecule type: protein

A:Residues: 19-40;133-144,'T',146-152;229-248 <IND>

C:Genetics:

A:Map position: 19

C:Keywords: egg yolk; homotrimer

F:132-133/Cleavage site: Lys-Asn (egg 30.5K cysteine proteinase) #status experimental

F:228-229/Cleavage site: Arg-Asp (egg 30.5K cysteine proteinase) #status experimental

Query Match

Best Local Similarity 23.5%; Score 502.5; DB 2; Length 559;

Matches 128; Conservative 63; Mismatches 154; Indels 47; Gaps 13;

QY 23 DLENEVNEVWNTSEIIINYGPSEEVETEDGYILLVNRIPYGRTH-ARSTGPRPV 81

DB 179 ETQRENEDFHLNATELLKKHOYPVEEHTVATDDGYHLTVLRIP--PTHQTRDDKKKPPVA 236

QY 82 YMOHALFADNAVLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDEKFWAF 141

DB 237 LUMHGLGSDADLLMGFSKSLAYLMDAGYDVWNGVGNKYSRSHVSKHPALNDFWKF 296

QY 142 SPDEMAKYDLPGVIDFIYVNTGQEKLYFIGHSLGTTIGFVAFSTMPPELAQRKMMFALGP 201

DB 297 SNDEIALHDLPAIDHVLDISQERLHYIGHSQGATTFEALMSQEPSYNEKIVSMHALSP 356

QY 202 TTSFYI-----PTGIFTRF-----LLPNSLIKAVFGTKFFLEDKKTTKAS 243

DB 357 IYMYNVRSPFRMTAPTSKEYQYIHDQVGHGAFEPGKHLETFTGGAAC-----REKLGC 411

QY 244 TKICNKKILWLICSEFMSLWAGSNKKNQSRMDVYMSHAPTGVSSVHNLHKLQLYHSDE 303

DB 412 RHVCNN-LNYVI-----SGINYNQDADIVPVVMAHLPAGTSARVKNKQVGNVASHD 462

QY 304 FRAYDWGNDADNKNHNSHPPIYDLTAMKVPTAIWAGGHV-LGTPOQDVARI---LPQI 359

DB 463 FRKYNAGET-NMKYVGASEPSYDLKSVSAPVNLV-HSHDAWLAHPDXVEKLQENLPV 520

QY 360 KSLSLVLSLLPWE---PTDFWVWGLDAPQRMF 389

DB 521 KQSFEV----PQQHFTDLDFQFSKAPDTVY 548

RESULT 13

T31611

hypothetical protein Y5088A.g - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T31611

R:Steward, C.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z21047

A:Accession: T31611

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1585 <WIL>

A:Cross-references: EMBL:AL117200; NID:el549770; PIDN:CAB55050.1; CESP:Y5088A.g

A:Experimental source: clone Y5088A

C:Genetics:

A:Gene: CESP:Y5088A.g

A:Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

Query Match 22.0%; Score 469.5; DB 2; Length 1585;

Best Local Similarity 31.6%; Pred. No. 4.1e-31; Indels 15; Gaps 7;

Matches 117; Conservative 67; Mismatches 171;

QY 31 EWMNTSEIIINYGPSEEVETEDGYILLVNRIPYGRTHARSTG--PRPVVYMQHALF 88

DB 20 EETLDAADTISHYGYTVEKHVYTTDDGYTVQLQIPVGRDDRSILGCSKRPVVEFMHGLF 79

QY 89 ADNAVWLENYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDKFWAFSDEWAK 148

DB 80 GSSYHFLNPSQSAAYIFADAGFDVWGLNGRTGYGLNHTFSFGVNFNFSLEYHSH 139

QY 149 YDLPGVIDFIYVNTGQEKLYFIGHSLGTTIGFVAFSTMPPELAQ-RIKKNFALGPTISFKY 207

DB 140 YDLROOIEYVLDYTRHESLFYVGHSGQTAVMFARLAEADVTWQSKIRVFFALGPTAGFMK 199

QY 208 PTGIFTRFELLPSNIIKAVF-----GTRGFFLEDDKTKIAS--TKICNKKILWLICSEFM 260

DB 200 PLMPPT---LLEENYLQALIQFALDQKFGILPVEIPRAIASKAFADFCSSKPPFTLCSAGF 256

QY 261 SLWAG-SNKKNNQSRMDVYMSHAPTGVSSVHNLHKLQLYHSDEFRAYDWGNDADNKH 319

DB 257 KVAAGIETLQGVNDSRIPILSHFPSATSTLLHWMQIFKYHELRRLDLGT-ARNLIAY 315

QY 320 NQSHPPYIDLTAMKVPTAIWAGGHVLTGPQDVARILPOIKSLSLVLSLLPWEPTFDFV 379

DB 316 GOKDAPRLEIGNIIAQTILYFSKDDQITDEVVDREIIMKMGPGGLIESYDLDFHFTDFEI 375

QY 380 WGLDAPQRMF 389

DB 376 LGLRATDEVY 385

RESULT 14

T39540

triglyceride lipase-cholesterol esterase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: T39540

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.

submitted to the EMBL Data Library, February 1998

A:Reference number: Z21862

A:Accession: T39540

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-443 <WOO>

A:Cross-references: EMBL:AL021748; PIDN:CAA16863.1; GSPDB:GN00067; SPDB:SPBC16A3.12c

A:Experimental source: strain 972h-; cosmid cl6A3

C:Genetics:

A:Gene: SPDB:SPBC16A3.12c

A:Map position: 2

A:Introns: 11/2; 152/3; 282/1; 398/3

C:Superfamily: triacylglycerol lipase, lingual

Query Match

Best Local Similarity 20.4%; Score 436; DB 2; Length 443;

Matches 116; Conservative 68; Mismatches 150; Indels 32; Gaps 12;

QY 35 NTSEIIINYGPSEEVETEDGYILLVNRIPYGRTHAR-STGPRPVVYMQHALFADNAY 93

DB 74 NIYEICEAFGYVEEHLVYRTQDNFILCHRI---THPKSQSHKREVYVCHHGLMTNSEL 129

QY 94 MLE-NYANGSLGFLADAGYDVWNGSRGNTWSRRHKTLSSETDKFWAFSDEWAKYDLP 152

DB 130 WVAVNESRSLPFFVLIESGYDWLGNRGNKYSRKHITYKPKDEBFNFWSLDDMAFMFDP 189

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:35:32 ; Search time 19 seconds
(without alignments)
862.271 Million cell updates/sec

Title: US-10-003-302-2

Perfect score: 2137

Sequence: 1 MWLLLTTCICGTLNAGG.....FDFVGLDAPQRMFSGNHNL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1091	51.1	399	1	LICH_HUMAN
2	1052	49.2	398	1	LIPG_HUMAN
3	1031	48.2	398	1	LIPG_CANFA
4	1022.5	47.8	395	1	LIPG_RAT
5	1015	47.5	397	1	LICH_RAT
6	982.5	46.0	397	1	LIPG_BOVIN
7	980.5	45.9	397	1	LICH_MOUSE
8	533	24.9	394	1	LIP3_DROME
9	486	22.7	439	1	LIP1_DROME
10	342.5	16.0	548	1	TGLI_YEAST
11	103.5	4.8	436	1	PAFA_CAVPO
12	102	4.8	349	1	HS2S_DROME
13	99.5	4.7	185	1	YCZH_BACSU
14	99	4.6	804	1	RIRI_PLAFG
15	97	4.5	277	1	BPHD_PSES1
16	96.5	4.5	879	1	YE07_MYCPN
17	94	4.4	445	1	SPR1_YEAST
18	93	4.4	444	1	PAFA_BOVIN
19	92.5	4.3	268	1	ESL2_MYCPN
20	91	4.3	1864	1	CGNS_RCMV
21	90.5	4.2	1680	1	CO5_MOUSE
22	90	4.2	404	1	Y432_SCHPO
23	89.5	4.2	428	1	YE63_SCHPO
24	89.5	4.2	910	1	SC15_YEAST
25	89	4.2	857	1	LOX3_SOYBN
26	88.5	4.1	423	1	P47A_CANBO
27	88.5	4.1	1046	1	K052_HUMAN
28	87	4.1	860	1	KDPP_MYCTU
29	87	4.1	1155	1	RPOB_BORBU
30	87	4.1	3744	1	YHP9_YEAST
31	86.5	4.0	441	1	PAFA_HUMAN
32	86.5	4.0	1409	1	HAP1_HAFIN
33	86	4.0	643	1	GYRB_MYCCA

RESULT 1

ID	LICH_HUMAN	STANDARD;	PRT;	399 AA.
AC	P38571: 016529; Q96EJO;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lysosomal acid lipase/cholesterol ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesterol ester hydrolase) (Sterol esterase) (Lipase A) (Cholesteryl esterase).			
GN	LIPA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 196-212; 277-297 AND 305-315.			
RX	MEDLINE=92042192; PubMed=1718995;			
RA	Anderson R.A., Sando G.N.;			
RT	"Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesterol ester hydrolase. Similarities to gastric and lingual lipases.";			
RL	J. Biol. Chem. 266:22479-22484(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=94155897; PubMed=8112342;			
RA	Ameis D., Merkel M., Eckerskorn C., Greten H.;			
RT	"Purification, characterization and molecular cloning of human hepatic lysosomal acid lipase.";			
RL	Eur. J. Biochem. 219:905-914(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96363957; PubMed=8725147;			
RA	Du H., Witte D.P., Grabowski G.A.;			
RT	"Tissue and cellular specific expression of murine lysosomal acid lipase mRNA and protein.";			
RL	J. Lipid Res. 37:937-949(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Strausberg R.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	VARIANT CSD/MD PRO-200.			
RX	MEDLINE=94195814; PubMed=8146180;			
RA	Anderson R.A., Byrum R.S., Coates P.M., Sando G.N.;			
RT	"Mutations at the lysosomal acid cholesterol ester hydrolase gene locus in Wolman disease.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994).			
RN	[6]			
RP	VARIANTS CSD ARG-129 AND PRO-129.			
RX	MEDLINE=98295576; PubMed=9633819;			
RA	Ries S., Buechler C., Schindler G., Aslanidis C., Gasche C., Jung N., Schambach A., Fehrer P., Vanier M.T., Belli D.C.,			

P03593 alfalfa mos
Q33654 staphylococ
Q07121 arthrobacte
Q07123 arthrobacte
P39985 saccharomyc
P19097 s fatty aci
Q9qzy8 cavia porce
P29016 homo sapien
O46051 drosophila
P81171 rickettsia
P32480 saccharomyc
P55895 homo sapien

ALIGNMENTS

RA Greten H., Schmitz G.;
RT "Different missense mutations in histidine-108 of lysosomal acid
RT lipase cause cholesteryl ester storage disease in unrelated compound
RT heterozygous and hemizygous individuals.";
RL Hum. Mutat. 12:44-51(1998).
CC -1- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
CC MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
CC MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION.
CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- DISEASE: DEFECTS IN LIPA ARE THE CAUSE OF THE SEVERE INFANTILE-
CC ONSET WOLMAN DISEASE (WD) AND THE Milder LATE-ONSET CHOLESTERYL
CC ESTER STORAGE DISEASE (CESD).
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M74775; AAB59519.1; -;
DR EMBL; U04285; AAB60327.1; -;
DR EMBL; U04286; AAB60327.1; JOINED.
DR EMBL; U04287; AAB60327.1; JOINED.
DR EMBL; U04288; AAB60327.1; JOINED.
DR EMBL; U04290; AAB60327.1; JOINED.
DR EMBL; U04291; AAB60327.1; JOINED.
DR EMBL; U04292; AAB60327.1; JOINED.
DR EMBL; U04293; AAB60327.1; JOINED.
DR EMBL; X76488; CAA54026.1; -;
DR EMBL; Z31690; CAA83495.1; -;
DR EMBL; U08464; AAB60328.1; -;
DR EMBL; BC012287; AAB12287.1; -;
DR PIR; A39315; A39315.
DR Genew; HGNC:6617; LIPA.
DR MIM; 278000; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser esters_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 399
FT
FT ACT_SITE 174
FT ACT_SITE 374
FT CARBOHYD 36
FT CARBOHYD 72
FT CARBOHYD 101
FT CARBOHYD 161
FT CARBOHYD 273
FT CARBOHYD 321
FT VARIANT 16
FT
FT VARIANT 129
FT
FT VARIANT 129
FT
FT VARIANT 200
FT
FT CONFLICT 23
FT CONFLICT 29
FT SEQUENCE 399 AA; 45415 MW; 55F27391306B609A CRC64;

Query Match 51.1%; Score 1091; DB 1; Length 399;
Best Local Similarity 53.3%; Pred. No. 3.7e-82;
Matches 210; Conservative 63; Mismatches 119; Indels 2; Gaps 2;
QY 2 MWLLTTTCLICGTTNAGGFLDLENEVNPVMTSEIIYNGYSEVEYVETEDGYILL 61
DB 3 MRLGLVCLVLPVHSEGGKLTAVDPETNMNYSIIISYWGFPSEYLVETEDGYILL 62
QY 62 VNIPIGYTHARSTGRPVVYMHAFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 63 LNIPIGHRNHSKDPKPVFLQGLLADSNWNTNLNSSLGFLADAGYDVWNGNSRG 122
QY 122 NTSRRHRTLSDEKFWAFSEDEMAKYDLPGVIDFIYVNTKQOEKLYFTGHSLGTIGFV 181
DB 123 NTSRRHRTLSVSDQEFWAFSEDEMAKYDLPGVIDFIYVNTKQOEKLYFTGHSLGTIGF 182
QY 182 ARSTPELAORIKMNFALPGTISFKYPTGIFTRFELLPSIIKAVFGKGFLEDKTKKI 241
DB 183 AFSPQPELAKRIKMFALGPVAVAFCTSPMAKGLRPLDHLIKDLFGDKEFLPQSAFLKW 242
QY 242 ASTKCNKILWLCSEFMSLWAGSNKKNQSDVYMSHAPTSSVHNIHLRIQLYHS 301
DB 243 LGTHVCTHVLKELCGNLCFLCGENRNLNNSRDVYTHSPAGTSVQNMHLHWSQAVKF 302
QY 302 DEFAYDMGNDADNMKNHNSHPPIYDITAMKVPTAINAGGHDVILGTPODVARILPQIKS 361
DB 303 QKQFAFDGSSAKNYFHYNQSPYPTYNVKDMLVPTAVMSGGHDLADVYDVNILLTQITN 362
QY 362 LSLVLSLPEWEPTDFVWGLDAPQPMFSGNHL 395
DB 363 LVFHES-IPWE-HLDFWGLDAPWRLNKIINL 394
RESULT 2
LIPG_HUMAN STANDARD; PRT; 398 AA.
AC AC P07098;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
DE lipase) (GL).
GN LIPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299724; PubMed=3304425;
RA Bodmer M.W., Angal S., Yarranton G.T., Harris T.J.R., Lyons A.,
RA King D.J., Pieroni G., Riviere C., Verger R., Lowe P.A.;
RT "Molecular cloning of a human gastric lipase and expression of the
RT enzyme in yeast.";
RT Biochim. Biophys. Acta 909:237-244(1987).
RL [2]
RN SEQUENCE OF 20-45.
RX MEDLINE=89325292; PubMed=2753032;
RA Bernbaeck S., Blaackberg L.;
RT "Human gastric lipase. The N-terminal tetrapeptide is essential for
RT lipid binding and lipase activity.";
RN Eur. J. Biochem. 182:495-499(1989).
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=99287897; PubMed=10358049;
RA Roussel A., Canaan S., Egloff M.P., Riviere M., Dupuis L., Verger R.,
RA Cambillau C.;
RT "Crystal structure of human gastric lipase and model of lysosomal
RT acid lipase, two lipolytic enzymes of medical interest.";
RJ J. Biol. Chem. 274:16995-17002(1999).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; X05997; CAA29413.1; -;
DR EMBL; X05997; CAA29414.1; ALT_INIT.
DR EMBL; A01046; CAA00125.1; -;
DR EMBL; A12714; CAA01053.1; -;
DR PIR; S04942; S04942.
DR PIR; S07145; S07145.
DR PDB; 1HLG; 15-MAR-00.
DR Genew; HGNC:6622; LIPF.
DR MIM; 601980; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 398 TRIACYLGLYCEROL LIPASE, GASTRIC.
FT ACT_SITE 172 172 CHARGE RELAY SYSTEM.
FT ACT_SITE 343 343 CHARGE RELAY SYSTEM.
FT ACT_SITE 372 372 CHARGE RELAY SYSTEM.
FT DISULFID 246 255
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .).
FT CARBOHYD 327 327 T -> A (IN DBSNP:814628).
FT VARIANT 161 161 /FTID=VAR_011947.
SQ SEQUENCE 398 AA; 45237 MW; CD3EE1621C014F0F CRC64;

Query Match 49.2%; Score 1052; DB 1; Length 398;
Best Local Similarity 50.4%; Pred. No. 5.8e-79;
Matches 196; Conservative 68; Mismatches 123; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGLNAGGFLDLENVNPEVMMNTSEIIYNGYPSSEYEVTTEDGYILL 61
Db 1 MWLLTASLSVLGTTGHLFGKLGPGSPFTVMTNISQMTITWGYPNBEEYVTTEDGYILE 60

Qy 62 VNRIPIYGRTHARSTGRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMMGNSRG 121
Db 61 VNRIPIYGKKNSTGRQPVVFLQGLLASATNWNLSNPNLSAFILADAGYDVWLGNSRG 120

Qy 122 NWSRRHKTLSSETDEKFWAFSDEMAYKDYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181
Db 121 NTWARRNLYYSPDSVEEFWAFSDEMAYKDYDLPATIDFIVKTKGQKQLHVYVGHSGQTTIGFI 180

Qy 182 AFTSMPELAQRKKNFALGPTISFKYPTGIFTREFLLPNSLIKAVGPKGFLEDDKTKI 241
Db 181 AFTSNPSLAKRIKIFYALPAPVATKYTKSLINKLRFVQSLFKIFGDKIYFPHNFFDQF 240

Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNNMQSRMDVYMSHAPTGGSSVHNLTHLKQLVHS 301
Db 241 LATEVCSREMLNLLCSNLFICGFSKNTSLRDVYLSHNPAGTSVQNNFHWTAQVKS 300

Qy 302 DEFRAIDNGNDADNMKNHNSQHPPIYDLTAMKVPTAIWAGHDVIGTQDVARILPQTKS 361
Db 301 GKFOAYDWGSPQNRMHYDQSPYPYNTAMNVPVAVNNGKDLIADPDQVGLLLPLKPN 360

Qy 362 LSLVLSLLEPEPTDFVWGLDAPQRFES 390
Db 361 L-IYHKEIPFYN-HLDFIWMADAPQEVYN 387

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RESULT 3
LIPG CANFA STANDARD; PRT; 398 AA.
AC P80035; 002857;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
DE lipase) (GL).
GN LIPF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Vaganay S., Joliff G., Bertaux O., Toselli E., Devignes M.D.,
RA Benicourt C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 20-59.
RA MEDLINE-92037652; PubMed-1935982;
RA Carriere F., Moreau H., Raphael V., Laugier R., Benicourt C.,
RA Junien J.-L., Verger R.;
RT "Purification and biochemical characterization of dog gastric
RT lipase."
RL Eur. J. Biochem. 202:75-83(1991).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y13899; CAA74198.1; -;
DR PIR; S19539; S19539.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 398 TRIACYLGLYCEROL LIPASE, GASTRIC.
FT ACT_SITE 172 172 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 372 372 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 I -> T (IN REF. 2).
SQ SEQUENCE 398 AA; 45130 MW; E04D62F7518E386C CRC64;

Query Match 48.2%; Score 1031; DB 1; Length 398;
Best Local Similarity 48.8%; Pred. No. 3.1e-77;
Matches 190; Conservative 72; Mismatches 125; Indels 2; Gaps 2;

Qy 2 MWLLTTTCLICGLNAGGFLDLENVNPEVMMNTSEIIYNGYPSSEYEVTTEDGYILL 61
Db 1 MWLLTASVSLTGLTGHFLGKLGHTPTNPTVMTNISQMTITWGYPAEYEVTTEDGYILG 60

Qy 62 VNRIPIYGRTHARSTGRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVMMGNSRG 121
Db 61 IDRPIYGRKNSENIGRRPVAFLOHGLLASATNWNLSNPNLSAFILADAGYDVWLGNSRG 120

Qy 122 NWSRRHKTLSSETDEKFWAFSDEMAYKDYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181
Db 122 NWSRRHKTLSSETDEKFWAFSDEMAYKDYDLPVDFIVNKTGQEKLYFIHSLGTTIGFV 181

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Db 121 NTWARRNLVYSPDSVEFWAFSDEMAKYDLPATIDILFKKTKQDQLHYVGHVSQGTIGFI 180
QY 182 AFSTPELAQRKMFALGPTISFYKPTGIFTRFFLLPSIIKAVFGTKGFLEDKKTKI 241
Db 181 AFSTNPKLAKRTYALAPVATVYKTELLNKLMLVPSFLEKLFNGKIFYPHFFDOF 240
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSDMDVYMSHAPTSSVHNHILHIKOLYS 301
Db 241 LATEVCSRETVLLCSNALFICGFTMLNLSRLDVLVSHNPAGTSSVQNLVHWSQAVKS 300
QY 302 DEFAYDAGNDADNKKHYNQSHPPYDILTKAMKVPYTAIWAGGHVGLTPODVARILPOIKS 361
Db 301 GRQFADFGSPVQNMHHYHMPYNTLDMHVPYAVWNGNDLLADPHDVLKSLKLPN 360
QY 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390
Db 361 L-IYHRKIPPYN-HLDFIWMADAPQAVYN 387
RESULT 4
LIPG_RAT STANDARD; PRT; 395 AA.
AC P04634;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, lingual precursor (EC 3.1.1.3) (Lingual
lipase).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215587; PubMed=3839077;
RA Doherty A.J.P., Bodner M.W., Angel S., Verger R., Riviere C.,
Lowe P.A., Lyons A., Emage J.S., Harris T.J.R.;
RT "Molecular cloning and nucleotide sequence of rat lingual lipase
cDNA".
RL Nucleic Acids Res. 13:1891-1903(1985).
CC -|- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
fatty acid anion.
CC -|- MISCELLANEOUS: LINGUAL LIPASE IS SECRETED BY THE SEROUS (VON
EBNER'S) GLANDS AT THE BACK OF THE RAT TONGUE.
CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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CC
CC EMBL; X02309; CAA26179.1; -;
CC DR EMBL; A01157; CAA00136.1; -;
CC PIR; A23045; LIRTT.
CC DR InterPro; IPR000073; Abhydrolase.
CC DR InterPro; IPR000734; Lipase.
CC DR InterPro; IPR000379; Ser_estrs_site.
CC DR Pfam; PF00561; abhydrolase; 1.
CC DR PROSITE; PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 395 TRIACYLGLYCEROL LIPASE, LINGUAL.
CC FT ACT_SITE 171 171 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 342 342 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 371 371 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT DISULFID 245 254 BY SIMILARITY.
CC FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 395 AA; 44588 MW; E601854A923522EA CRC64;
Query Match 47.8%; Score 1022.5; DB 1; Length 395;
Best Local Similarity 48.4%; Pred. No. 1.5e-76;
Matches 192; Conservative 67; Mismatches 119; Indels 19; Gaps 3;
QY 2 MWLLLTITTC-----ICGTLNAGGFLDLENVNPVMMNTSEIIIVNGYPSSEYEV 53
Db 1 MWLLLTITSVISFGGAHGLFGKLGPG-----NPEANMNIISOMITYWGYPCOEYEV 51
QY 54 TEDGQVILLVNRITPGYRTHARSTGPRPVVYMOHALFADNAYWLENYANGSIGFLADAGVD 113
Db 52 TEDGQVILGYIRPHGKNNSSENGKRPVYVYLQHLGLASATNWNLANPNNSLAFMLADAGVD 111
QY 114 VMNGSRGNTWSRRHKTLSSETDEKFWAFSDEMAKYDLPVDFIVNKTQGEKLYFVGH 173
Db 112 VMNGSRGNTWSRKNNVYSPDSVEFWAFSDEMAKYDLPATINFIQKTQGEKIHVGH 171
QY 174 LGTTGFAVSTMPELAQRKMFALGPTISFYKPTGIFTRFFLLPSIIKAVFGTKGF 233
Db 172 QGTTGFAVSTNPTLAKKIKTFYALAPVATVYKTSPLKISFIPTFLKLMFGKKMFL 231
QY 234 LEDKTKTASTKICNNKILWLCSEFMSLWAGSNKNNQSDMDVYMSHAPTSSVHNH 293
Db 232 PHTYFDDFLGTEVCSREVLDDLCNTLFIKFGDKKLNVSDFVYLGHNPAQTSVQDFL 291
QY 294 HIKOLYHSDFRAYDGNADNKKHYNQSHPPYDILTKAMKVPYTAIWAGGHVGLTPODVA 353
Db 292 HWAQLVRSKGFQAFNWGSPSQNNLHYNQKTPPEYDVSAMTVPVAVWNGNDILADQDVA 351
QY 354 RILPOIKSLVLSLLPEWPTDFVWGLDAPQRMFS 390
Db 352 MLLPKLSNLLPHKKEILA--YNHLDFIWMADAPQEVYN 386
RESULT 5
LICH_RAT STANDARD; PRT; 397 AA.
AC Q64194;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysosomal acid lipase/cholesteryl ester hydrolase precursor
DE (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol
esterase) (Lipase A) (Cholesteryl esterase).
GN LIPA OR LAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96129534; PubMed=8576647;
RA Nakagawa H., Matsubara S., Kuriyama M., Yoshidome H., Fujiyama J.,
Yoshida H., Osame M.;
RT "Cloning of rat lysosomal acid lipase cDNA and identification of the
RT mutation in the rat model of Wolman's disease".
RL J. Lipid Res. 36:2212-2218(1995).
CC -|- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
CC MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
CC MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (By
CC similarity).
CC -|- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -|- SUBCELLULAR LOCATION: Lysosomal.
CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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DR EMBL; S81497; AAB36043.2; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
KW PROSITE; PS00120; LIPASE_SER; Glycoprotein; Signal; Lysosome.
FT SIGNAL 1 19
FT CHAIN 20 397
FT LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER
FT HYDROLASE.
FT ACT_SITE 172 372
FT ACT_SITE 372 372
FT CARBOHYD 34 34
FT CARBOHYD 99 99
FT CARBOHYD 159 159
FT CARBOHYD 271 271
FT CARBOHYD 319 319
SQ SEQUENCE 397 AA; 45186 MW; 97A38595A0523947 CRC64;

Query Match 47.5%; Score 1015; DB 1; Length 397;
Best Local Similarity 49.1%; Pred. No. 6.3e-76;
Matches 192; Conservative 76; Mismatches 117; Indels 6; Gaps 4;

Qy 2 MWLLTTTCLICGLNAGGFLDLENEVPEVMMNTSEIIINYGPSEYEVTTEDGYILL 61
Db 1 MQLLRVICFVVGILLGGPTGTTISAVDPEANMNVTEIIMHWGYP--EHSVQTGDGYTLG 58
Qy 62 VNRIPIYGRTHARSGPRPVYMQ--HALFADNAYWLENYANGSLGFLADAGYDVMWGS 119
Db 59 VHRIPHGRKKNQFDGKPPVYQWRHGFGLADSSNWNVDNNSNGLFLADAGYDVMWGS 118
Qy 120 RGNTWSRRHKTLSDEKFWAFSDEMAKYDLPVDFIVNKTGOEKLYFGTGLGTTIG 179
Db 119 RGNTWSRRHKTLSVQDEYFAFDEMAKYDLPASINVLNKTGOEQLYNYGHSGQTIG 178
Qy 180 FVASTWPELAQRKIMNFALGPTISFYKPTGIFTRFLLPNSIIKAVFGTKGFLEDKKT 239
Db 179 FIAFSOMPELAKVKMFALAPVLSNFASGPMYKGLRPLDLLLEDLFGQKFLPQSAMV 238
Qy 240 KIASTKCNKILWLCSEFMSLWAGSKKNQSDMDVYMSHAPTSSSVNHLIKOLY 299
Db 239 KWLSTHICTHVIMKELCANIEFLICGNEKNLNSRVDVYTHCPAGTSVQNMVHWTOV 298
Qy 300 HSDEFAYDNGNDADNMKNHYNOSHPIYDLTAMKVPTAIMAGGHVDVLGTPQDVARILPQI 359
Db 299 KYHKLQAFDMSGSSDKNYFHYNQSYPLYSIKDMQLPTALWSSGKDLADTSDINILLTEI 358
Qy 360 KSLSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
Db 359 PTL-VYHKNIPEWD-HLDFIWGLDAPWRLYN 387

RESULT 6
LIPC_BOVIN STANDARD; PRT; 397 AA.
AC Q29458;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triacylglycerol lipase, pregastric precursor (EC 3.1.1.3) (Pregastric
DE lipase) (GL) (Pregastric esterase) (PGE).
GN LIPF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RN SEQUENCE FROM N.A.
RC TISSUP-Tongue serous gland;
RX MEDLINE-95011625; PubMed-7926811;
RA Timmermans M.J.O., Kupers L.P., Teuchy H.;
RT "The cDNA sequence encoding bovine pregastric esterase";
RL Gene 147:259-262(1994).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O -> diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC

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CC EMBL; L26319; AAA57037.1; -;
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 397
FT ACT_SITE 171 171
FT ACT_SITE 371 371
FT CARBOHYD 33 33
FT CARBOHYD 270 270
FT CARBOHYD 326 326
SQ SEQUENCE 397 AA; 45231 MW; F68977DED585EE36 CRC64;

Query Match 46.0%; Score 982.5; DB 1; Length 397;
Best Local Similarity 47.3%; Pred. No. 2.9e-73;
Matches 184; Conservative 72; Mismatches 130; Indels 3; Gaps 3;

Qy 2 MWLLTTTCLICGLNAGGFLDLENEVPEVMMNTSEIIINYGPSEYEVTTEDGYILL 61
Db 1 MWLLTVTCFTHMSGNAFCFLG-KIAKNPEASMNVSQMSIYWGYPSEMHKVVITADGYILQ 59
Qy 62 VNRIPIYGRTHARSGPRPVYMQ--HALFADNAYWLENYANGSLGFLADAGYDVMWGSRG 121
Db 60 VYRIPHGRKNNHNLGQRPVFLQHGLGSATNWSLNPKNSLGLFLADAGYDVLGNSRG 119
Qy 122 NTWSRRHKTLSDEKFWAFSDEMAKYDLPVDFIVNKTGOEKLYFGTGLGTTIGV 181
Db 120 NTWAEHLIYSPDSPEFWAFSDEMAEYDLPSTIDFILRRTGQKKLVHVGHSQGTIGFI 179
Qy 182 AFSTMPPELAQRKIMNFALGPTISFYKPTGIFTRFLLPNSIIKAVFGTKGFLEDKKTKI 241
Db 180 AFSTPTLAERIKVYALAPVATVKYTSKLENKIALIPHEFLFKIIFGDKMFPHTFLQOF 239
Qy 242 ASTKICNKNILWLCSEFMSLWAGSKKNQSDMDVYMSHAPTSSSVNHLIKOLXHS 301
Db 240 LGVSCSRETLDVLCCKNALFAITGVDNKNENMSRLDVIHNPACTSVQNTLHWQAVKS 299
Qy 302 DEFAYDNGNDADNMKNHYNOSHPIYDLTAMKVPTAIMAGGHVDVLGTPQDVARILPQKS 361
Db 300 GKFOAFOWGAPYQNLHMYHQPTPIYNTAMNVPYAVWSADNLLADPDQDVFLLSLSN 359
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMFS 390
Db 360 L-IYHKEIPNPN-HLDFIWAMDAPQEVYN 386

RESULT 7
LICH_MOUSE STANDARD; PRT; 397 AA.
ID LICH_MOUSE
AC Q9Z0M5;
DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Lysosomal acid lipase/cholesterol ester hydrolase precursor
 DE (EC 3.1.1.13) (LAL) (Acid cholesterol ester hydrolase) (Sterol
 DE esterase) (Lipase A) (Cholesterol esterase).
 OS LIPA OR Lip1.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
 RA MEDLINE=96363957; PubMed=8725147;
 RA Du H., Witte D.P., Grabowski G.A.;
 RT "Tissue and cellular specific expression of murine lysosomal acid
 RT lipase mRNA and protein.";
 RL J. Lipid Res. 37:937-949(1996).
 CC -|- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL
 CC ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-
 CC MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN
 CC MEDIATING THE EFFECT OF LDL (LOW DENSITY LIPOPROTEIN) UPTAKE ON
 CC SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION
 CC OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (BY
 CC similarity).
 CC -|- CATALYTIC ACTIVITY: A sterol ester + H(2)O -> a sterol + a fatty
 CC acid.
 CC -|- SUBCELLULAR LOCATION: Lysosomal.
 CC -|- TISSUE SPECIFICITY: Expressed at low levels in most tissues. High
 CC level expression is found in hepatocytes and splenic and thymic
 CC cells. Very high level expression is observed in cells of the
 CC small intestinal villi, the zona fasciculata and reticularis of
 CC the adrenal cortex, pancreatic acini, and renal tubular
 CC epithelium.
 CC -|- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; 231689; CAA83494.1; --
 DR MGD; MGI:96789; Lip1.
 DR InterPro; IPR000073; Abhydrolase.
 DR InterPro; IPR000734; Lipase.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR Pfam; PF00561; abhydrolase; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome.
 FT SIGNAL 1 19
 FT CHAIN 20 397
 FT ACT_SITE 172 172
 FT ACT_SITE 372 372
 FT CARBOHYD 34 34
 FT CARBOHYD 99 99
 FT CARBOHYD 159 159
 FT CARBOHYD 271 271
 FT CARBOHYD 319 319
 FT SEQUENCE 397 AA; 45551 MW; F866C39E1CCFA91F CRC64;
 Query Match 45.9%; Score 980.5; DB 1; Length 397;
 Best Local Similarity 49.2%; Pred. No. 4.3e-73;
 Matches 185; Conservative 68; Mismatches 112; Indels 11; Gaps 3;
 QY 14 GTLNAGGFLDLENVNPDEWMTSTIIYNGYPSBEYVTTEDGVLILNRPYGRTHAR 73
 DB 22 GTVSA-----VDPEVNMVNTIIRMGVGPGEHSVLTGDGVLISIHRIIPGWNHNF 72
 QY 74 STGPRPVVYMQHALFADNAYLWENANGSLGFLADAGVDVWNGSRGNTWRRKTLSE 133

DB 73 GKGPRPVYLQHCILLADSSNWVTNIDNSLGLLADRGFDVWNGSRGNTWRLKHTLSV 132
 QY 134 TDEKWFASFDEMAKYDLPVGFIDFIVNKTQBEKLYFIGHSLGTTIGFVAFSTMPLEAQR 193
 DB 133 SQDEFWAFSDEMAKYDLPASINYILNKTQBEQIYVVGHSQCGTIGFIAFSQMPLEAK 192
 QY 194 KNFALGPTIISFKYPTGTFTRFELPLNSIKAVFGTKGFFLEDKKTKTASTKCNKILW 253
 DB 193 KMFLLAPVLSLNFASGPLLQGLRPLDKMFKQKQFQPQSAKMLKWLISIVCHTHVIMK 252
 QY 254 LICSEFMSLWAGSNKKNQSMQMDVYMSHAPTGSVHNILHIKLYHSDEFDAYDGNDA 313
 DB 253 ELCAVNFELLCGFNEKNLMSRDVYTHCPAELLVONMLHNGQVFKYRKLQAFDWSSE 312
 QY 314 DMKHYNOSHPPFYDLTAMKVPTAIWAGHDVLGTPQDVARILPOIKSLSLSLSLLPEWE 373
 DB 313 KNYFHYNSQFPPSYINKMRLPTALWSGGROWLADINDITILLTQTPKL-VYHKNIPEWD 371
 QY 374 PTFDFVWGLDAPQRMF 389
 DB 372 -HLDFIWLGLDAPWKLY 386
 RESULT 8
 LIP3_DROME STANDARD; PRT; 394 AA.
 AC 046108;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lipase 3 precursor (EC 3.1.1.-).
 GN LIP3 OR CG8823.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7427;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=98227315; PubMed=9566193;
 RA Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C.;
 RT "The Drosophila melanogaster lipase homologs: a gene family with
 RT tissue and developmental specific expression.";
 RL J. Mol. Biol. 276:877-885(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fogle C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -!- TISSUE SPECIFICITY: FAT BODY.
CC -!- DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
CC LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
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CC -----
DR EMBL: Y14367; CAA74737.1; -.-
DR EMBL: AE030369; AAF54935.1; -.-
DR FlyBase: FBgn023495; Lip3.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase_1.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Signal; glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 394 LIPASE 3.
FT ACT_SITE 164 164 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 369 369 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 394 AA; 44901 MW; A718D1D743673802 CRC64;

Query Match 24.9%; Score 533; DB 1; Length 394;
Best Local Similarity 33.4%; Pred. No. 2.2e-36;
Matches 118; Conservative 77; Mismatches 148; Indels 10; Gaps 8;

Qy 43 NGYSPSEVEVTEDGYILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGS 102
Db 35 DGYPMERHEVVTSDNYILTMHRIPYSPKGTSSN-RPVAFLMHGMLSSSDWLMGPERS 93
Qy 103 LGFLLADAGYDVWNCNRCNTWTSRRHKTLSLTDKFAFSEDEWAKYDLPGVDFIVNKT 162
Db 94 LAYMLADAGYDVWNGNRAGNTYSKAHKYPTWYQIFWNFNFWNMGVDPVAMIDYVLAKT 153
Qy 163 QGEKLYFICHSIGLTIGVAFSTMPELAQRIKMFALCPTI---SFKYP-TGIFTRFPFL 218
Db 154 GOQVQVYVGHSGQTVYLVWYSEPEYNDKLSAHLGLPAAVMGNMKSPLTRAPILGQ 213
Qy 219 PMSIKAVFGTKGFLEDKTKYIASTKICNNKILWL-ICSEFMSLWAGSNKKNNQSRMD 277
Db 214 PNAIVE-VCGSMEFSPNSKFKQDLGIEMCQATSPYADMCANEIFLGGYDTEQLDYELLE 272
Qy 278 VYMSHAPGSSVHNLHLKQLYHSDPEFRAYDNGDADNKKHYNOSHPIYDLTAMKVPTA 337
Db 273 HIKATSPAGASVQNLHFCQYNSGKFRKFDY-TALRNPYEGYGFPPDYKLKNAKAPVL 331
Qy 338 IWAGGHVGLGTPQDVARLTLPKISLSL-VLSLLPEWETPFDVNGLDAPQRMF 389
Db 332 LIYGANDWMCVDSVRKLRDELNPALDYLVPFEKW-AHLDFIWGTAKRYVY 383

----- RESULT 9
LIPL_DROME STANDARD; PRT; 439 AA.
ID LIPL_DROME Q9VNR6;
AC 046107; Q9VNR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipase 1 precursor (EC 3.1.1.-).
DE LIPL OR C67279.
GN *Drosophila melanogaster* (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE OF 7-433 FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=98227315; PubMed=9566193;
RA Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C.;
RT "The *Drosophila melanogaster* lipase homologs: a gene family with
RL tissue and developmental specific expression.";
RL J. Mol. Biol. 276:877-885(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brattton R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes N., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flocker C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: COULD BE A DIGESTIVE ENZYME.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
CC LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
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DR EMBL; Y14366; CAA74736.1; -;
DR EMBL; AE003629; AAF52994.1; -;
DR FlyBase; FBgn0023496; Lip1.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
KW Hydrolase; Lipid degradation; Signal; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 439
FT LIPASE 1.
FT DOMAIN 30 44
FT ACT_SITE 197 197
FT ACT_SITE 393 393
FT ACT_SITE 393 393
FT CARBOHYD 124 124
FT CARBOHYD 151 151
FT CARBOHYD 346 346
FT CARBOHYD 379 379
FT CARBOHYD 426 426
FT CARBOHYD 10 10
FT CONFLICT 213 213
FT CONFLICT 412 412
FT CONFLICT 412 412
SQ SEQUENCE 439 AA; 50660 MW; 9E32E20BEAE93E3F CRC64;

Query Match 22.7%; Score 486; DB 1; Length 439;
Best Local Similarity 30.1%; Pred. No. 1.8e-32;
Matches 127; Conservative 71; Mismatches 170; Indels 54; Gaps 10;

QY 1 MWMLLLTTTCLICGTLNA---GGFLELNE-----VNPVVM 34
DB 7 MQLLLGLGVFISRIQOLIGGEDEDEDEEEESVEDTPEDLQRKNIKQDSTL 66
QY 35 NTSEIIYNGYPSSEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVVMQHALFADNAYW 94
DB 67 SVDKLIAGYGESEVHHVTTEDGYILLTWHR-----RKQAPPFL-LQHLVDSSAGF 118
QY 95 LENYANGSLGFLADAGYDVMGNSRGNTWSRRHKTSETDEKFWAFSDEMAYDLPGV 154
DB 119 VVMGPNVSLAYLLADHNDVWLGNARGNRYSRNHTTLPDDESKFWDFSWHEIGMYDLPAM 178
QY 155 IDFIYNTKQEKLYTIGHSGLTTCIGFVAFSTMPPELAQRKKNFALGPTISER-----YP 208
DB 179 IDHLVKTGTFPKLHAGHSQGTCTFFVCMSPAYNDKVMQALAPAVYAKETEDHPYI 238
QY 209 TGIFTRFLLPNSIIKAVFGTKGFFLEDKTKIASTKICNNKILICSEFMSLWAGSNK 268
DB 239 RAISLYFSLVSGSSIREMFENGFEEL---CRMTEETERLICIEAVFGIV-----GRNW 287
QY 269 KNNQSRMDVMYSHAPTSSVINLIHKLHSDFRAYDNGNDADNKKHYNQSHPIPYD 328
DB 288 NEFNKMFEPVILGHYPAGVAAQVAFHFIQIKSGRFAPYSYSSN-KNQLYRDHLPPRYN 346
QY 329 LFAMKVPATAGGHDVLTGTPQDVARILPQIKSLSLVLSLPEWE-PTFDVFWGLDAPOR 387
DB 347 LSLVTVPTFVYVYSTNDLLCHPKADVESMCDGIGNVT-GKYLVPQKEFNHDFLWADVRKM 405
QY 388 MF 389
DB 406 LY 407

RESULT 10
TGLL_YEAST STANDARD; PRT; 548 AA.
AC P34163;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Triglyceride lipase-cholesterol esterase (EC 3.1.1.1.-).
GN TGL1 OR YKL140W OR YKL5.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92245761; PubMed=1574929;
RA Abraham P.R., Mulder A., Van't Riet J., Planta R.J., Raue H.A.;
RT "Molecular cloning and physical analysis of an 8.2 kb segment of
RT chromosome XI of Saccharomyces cerevisiae reveals five tightly linked
RT genes.";
RL Yeast 8:227-238(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY.

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DR EMBL; Z25464; CAA80958.1; -;
DR EMBL; Z28140; CAA81981.1; -;
DR PIR; S37969; S37969.
DR PIR; S39000; S39000.
DR SGD; S0001623; TGL1.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
KW Hydrolase; Lipid degradation.
SQ SEQUENCE 548 AA; 62979 MW; 32D1F230701CB083 CRC64;

Query Match 16.0%; Score 342.5; DB 1; Length 548;
Best Local Similarity 29.6%; Pred. No. 1.4e-20;
Matches 107; Conservative 63; Mismatches 133; Indels 59; Gaps 13;
QY 48 BEYEVTTEDGYILLVNRIPYGRTHARSTGPRPVVMQHALFADNAYW---LENYANGSLG 104
DB 78 EDHLVRTEDNYILTLHRIP---PISKRNFNKVVYLHGLLMCSVDWCCNIERHKN--LP 132
QY 105 FLADAGYDVMGNSRGNTWSRRHKTSETDEKFWAFSDEMAYDLPQVIDFVNTGQ 164
DB 133 FVLHDLGYDVMGNNRGNKYSTAHLNKKPKSNKFWDFSIDEFAFFDIPNSIEFILDITKV 192
QY 165 EKLFIHSLGTTIGFVAFSTMPPELAQRKKNFALGPTISFKYPTGIFTRFLLPNSIIF 224
DB 193 DKVICIGFSQSAQMAFAFSEKLNKRVSHFIALAPAMT---PKGLHNR---IVDTLAK 246
QY 225 AVFGTKGFFLEDKTKIASTKICN-----NKLWLCSEFMSLWAGSNKK 269
DB 247 SSPGFMFLFF-GRKVLPSAVIQRTLHPTLFLNCLIDIANKILF-----NWK 292
QY 270 NNNQSRMDVMYSHAP--TGSSVHNLIHKLHSDFRAYDNGNDADNKKHYNQSHPIPYD 322
DB 293 SFNLPKROKIASYAKLYSTTSVKSVHWFQILRSQKQFQF---ESDNNLNLSTRPYQIA 349
QY 323 HPPIYDLTAMKVPTAIGAGHDVLTGTPQDVARILPQIKSLSLVLSLPEWEPTFDVFWGL 382
DB 350 NFP--TRTNKIPILLIYGGIDSLVIDVMKNLP-----FNSVFDVKVDNYEHLDLINCK 403
QY 383 DA 384
DB 404 DA 405

108	QY	-----ADAGYDVWMCNSRGN-TWSRRHKTLSSTDEK-----FWAPS 147
177	DB	VEHRDESAAATYYFQDAPAAEASNSWIYKCNLETSRTEERKQRLRGQEGCSQAQLSLLS 236
143	QY	FDE-----MAKYDLPGVIDFIVNKTGQEKLYFICHLSLGTGTGFAVAFSTMPELAQRIKMPA 198
237	DB	IDGEPYKVVLDLNFIDQIKLGSLSDESKVAIIIGHSEFG---GATVIOTLSE-DQRFRCGTA 292
199	QY	LQPTISFYKPTG-----IFTRFFLLPNSIIKAVFGTK-----GFFLEDKTKTKIASTK 245
293	DB	LDP-----WMPPEVGVDHVKIPQPLFFINSEYFQSANDTKKIEKFYQPKQKRMKIAVK 345
RESULT 12		
HSZS-DROME		
ID	IC	HSZS-DROME STANDARD; PRT; 349 AA.
AD	AD	P25722; Q9VIW4;
DT	DT	01-MAY-1992 (Rel. 22, Created)
DT	DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	DE	Heparin sulfato O-sulfotransferase (EC 2.8.2.-).
GN	GN	HS2ST OR CG10234.
OS	OS	Drosophila melanogaster (Fruit fly).
OC	OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC	OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX	OX	NCBI_TaxID=7227;
RP	RP	[1]
RP	RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP	RP	STRAIN=Oregon-R;
RC	RC	MEDLINE=92038937; PubMed=1936954;
RA	RA	Powers P.A.; Ganetzky B.;
RT	RT	"On the components of segregation distortion in <i>Drosophila</i>
RT	RT	<i>melanogaster</i> . V. Molecular analysis of the <i>Sd</i> locus.";
RRL	RRL	Genetics 129:133-144(1991).
RC	RC	[2]
RC	RC	SEQUENCE FROM N.A.
RC	RC	STRAIN=Berkley;
RC	RC	MEDLINE=20196006; PubMed=10731132;
RA	RA	Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	RA	Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	RA	Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA	RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA	RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	RA	Hosdin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	RA	Jatani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	RA	Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA	RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	RA	Nei S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA	RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	RA	Reinartz K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA	RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Query Match 4.7%; Score 99.5; DB 1; Length 185;
Best Local Similarity 27.2%; Pred. No. 0.31;
Matches 31; Conservative 23; Mismatches 49; Indels 11; Gaps 4;

Qy 77 PRPVVYMOHALFADNAYWLENYANGSLGFLADAGYVWMGNSRGNTWSRRHKTLSRTDE 136
D 3 KPLVILAEIYGVNSHMK-----MGRLIKMAGYDVLTPNLLGED---EYVTLKEKT 53

Qy 137 KFWAFSDFEMAKYDLPGLVIDFVNKTQGEKLYFGHSGTGTIGFVAFSTMPELA 190
D 54 AYEQFTKRLKTG-ETIIQPIVQIRAGRHIFVGFSGVGTIANWKC-SSMEPVS 105

RESULT 14
ID RIR1_PLAFG STANDARD; PRT; 804 AA.
AC P50647;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonucleoside-diphosphate reductase large chain (EC 1.17.4.1)
DE (Ribonucleotide reductase R1 subunit).
GN RNR1.
OS Plasmodium falciparum (isolate FCR-3 / Gambia).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5838;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94022359; PubMed=8415692;
RA Rubin H., Salem J.S., Li L.S., Yang F.D., Mama S., Wang Z.M.,
RA Fisher A., Hamann C.S., Cooperman B.S.;
RT "Cloning, sequence determination, and regulation of the
RT ribonucleotide reductase subunits from Plasmodium falciparum: a
RT target for antimalarial therapy";
RT Proc. Natl. Acad. Sci. U.S.A. 90:9280-9284 (1993).
RL
CC -1- FUNCTION: PROVIDES THE PRECURSORS NECESSARY FOR DNA SYNTHESIS.
CC -1- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized
CC thiorodoxin + H(2)O = ribonucleoside diphosphate + reduced
CC thiorodoxin.
CC -1- PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
CC LARGE CHAIN FAMILY.

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EMBL; AF205580; AAA29755.1; -
InterPro; IPR005144; ATP.
DR InterPro; IPR00788; Ribonucleo.red.
DR Pfam; PF00317; ribonuc_red.lg; 1.
DR Pfam; PF02867; ribonuc_red.lg; 1.
DR Pfam; PF03477; ATP-cone; 1.
DR PRINTS; P01183; RIBODTASEM1.
DR PROSITE; PS00089; RIBORED.LARGE; 1.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 804 AA; 92402 MW; 8D3C70EA2ED0A6E9 CRC64;

Query Match 4.6%; Score 99; DB 1; Length 804;
Best Local Similarity 21.7%; Pred. No. 2.2;
Matches 71; Conservative 50; Mismatches 94; Indels 112; Gaps 19;

Qy 21 FLDLEN-----EYNPEVMTSETIIYNGVPSSEYEVTT-----EDGY 58
D 452 FVLEKEEFNKLYEIKITIRNLDKIERNYIPVKEAKTSNTRHRPIGTIGVGLADTF 511

Qy 59 ILLVNRIPYGRTHARSTGPRPVVYMOHALFADNAYWL-----ENY--ANGSLGFLADAG 111

Db 512 MLL--RYLYESDAAKELNKRIVETMYAALEMSVDWLOGSPYESYQSGPSQGL----Q 565
Qy 112 YDVWNGNSRGNTWSRRHKTLSRTDEKFWAFSDFEMAKYDLPGLVIDFVNKTQGEKLYFG 171
D 566 FDMN-----AKVDNKYW--DWDE-----LKLKTAKTGRNLLLL- 598
Qy 172 HSLGTTIGFVAFSTMPELAQRKIMNFALGPTISFK-YPTGIFTR-----FFLLPNSIHK 224
D 599 -----APMTAS-----TSQILGNSESPEPTSYNIYRRVLSGEFFVNPVPHLLK 642
Qy 225 AVFGTKGFFLEDKTKYIASTKICNN-----IAHNGSIQYI--SEIPDDLKELYKTYWEIKQKNIIDMAADR 697
D 643 DLF-DRGLWDEDMKQOL-----IAHNGSIQYI--SEIPDDLKELYKTYWEIKQKNIIDMAADR 697
Qy 268 KKNMNSR-MDVYMSHAPTG---SSVH 290
D 698 GYFIDQSOSLNIYI-QKFTFAKLSSMH 723

RESULT 15
BPHD_PSES1 STANDARD; PRT; 277 AA.
ID BPHD_PSES1
AC PI7548;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-).
GN BPHD.
OS Pseudomonas sp. (strain KKS102).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=307;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89213965; PubMed=2540155;
RA Kimbara K., Hashimoto T., Fukuda M., Koana T., Takagi M., Oishi M.,
RA Yano K.;
RT "Cloning and sequencing of two tandem genes involved in degradation
RT of 2,3-dihydroxybiphenyl to benzoic acid in the polychlorinated
RT biphenyl-degrading soil bacterium Pseudomonas sp. strain KKS102";
RT J. Bacteriol. 171:2740-2747 (1989).
RL
CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS
CC (PCB) TO BENZOIC ACID AND CHLOROBENZOIC ACIDS.
CC -1- SIMILARITY: STRONG, TO E.COLI MHPC.

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EMBL; M26433; AAA25751.1; -
DR PIR; B32312; ESPSSK.
DR InterPro; IPR003089; AB_hydrolase.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Aromatic hydrocarbons catabolism; Hydrolase.
FT ACT_SITE 112 112 BY SIMILARITY.
SQ SEQUENCE 277 AA; 30253 MW; E0C7496186818D1E CRC64;

Query Match 4.5%; Score 97; DB 1; Length 277;
Best Local Similarity 20.5%; Pred. No. 0.84;
Matches 68; Conservative 39; Mismatches 111; Indels 114; Gaps 15;

Qy 69 RTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYVWMGNSRGNTWSRRH 128
D 24 RIHLNDAGQGERVIMLHGCGPGAGGWSNYRN--IG-PFEVAGYKVLPLDAPG----- 73

Qy 129 KTLSETDEKFWAFSDFE-----MAKYDLPGLVIDFVNKTQGEKLYFGHSLGTTIGFVAFS 184

Db 74 ---FNKSD---TVVMDQRLYNARSVKGMMDVL-----GIEKAHLYGNSMG---GAGALN 120
QY 185 TWPDLAQRIKMNFAFGPTTISEKYPTGIFTRFF-LLPNSIIKAVFGTKGFFLEDKKTIAS 243
Db 121 FALYPERTGKILMG-----PGLGNSLFTAMPMEGIKLLF----- 157
QY 244 TKICNNKILWLICSEFMSLWAGSNKKNMQSRMDVYMSHAPTGSSVHNILHIKQLYHSDE 303
Db 158 -----KLYAEPSETLKQ-----MLNVFLFDQSVITDE 185
QY 304 FRAYDGNADNKKHYNQSHPIYDLTAMKYPTAIWAGGHDVLGTPQDVARILPOIKSLS 363
Db 186 LLQGRWANTORNPEHLKN-----FILSAQKVPLSAW-----DVSARLGEIKAKT 229
QY 364 LVLSLLPEWEPTDFVWGLDAPQRMFSGNNHL 395
Db 230 LV-----TWGRD--DRFVPLDHGL 246

Search completed: April 2, 2003, 16:41:25
Job time : 24 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 16:38:33 ; Search time 94 Seconds
(without alignments)
865.836 Million cell updates/sec

Title: US-10-003-302-2.

Perfect score: 2137

Sequence: 1 MMWLLTTTLCIGTLNAGG.....FDEWGLDAPQRMFSGNHNL 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059.5	49.6	395	11 Q9D798	Q9D798 mus musculus
2	1058.5	49.5	395	11 Q9D6T5	Q9D6T5 mus musculus
3	1057.5	49.5	395	11 Q9C9P7	Q9C9P7 mus musculus
4	1056.5	49.4	395	11 Q9D6Q6	Q9D6Q6 mus musculus
5	1056.5	49.4	395	11 Q9D6P3	Q9D6P3 mus musculus
6	1055.5	49.4	395	11 Q9D6X0	Q9D6X0 mus musculus
7	1055.5	49.4	395	11 Q9D6L9	Q9D6L9 mus musculus
8	1053.5	49.3	395	11 Q9D7C5	Q9D7C5 mus musculus
9	1052.5	49.3	395	11 Q9D767	Q9D767 mus musculus
10	1050.5	49.2	395	11 Q9C9P8	Q9C9P8 mus musculus
11	1049.5	49.1	395	11 Q9D760	Q9D760 mus musculus
12	1048.5	49.1	395	11 Q9D766	Q9D766 mus musculus
13	1048.5	49.1	395	11 Q9D6S5	Q9D6S5 mus musculus
14	1046.5	49.0	395	11 Q9D796	Q9D796 mus musculus
15	1045.5	48.9	395	11 Q9D6Q3	Q9D6Q3 mus musculus
16	1045.5	48.9	395	11 Q9D6N8	Q9D6N8 mus musculus

17	1045.5	48.9	395	11	Q9D6L1	Q9D6L1 mus musculus
18	1043.5	48.8	395	11	Q9D6M9	Q9D6M9 mus musculus
19	1040.5	48.7	395	11	Q9D6Q2	Q9D6Q2 mus musculus
20	995	46.6	374	4	Q96LG2	Q96LG2 homo sapien
21	663.5	31.0	405	5	Q93789	Q93789 caenorhabdi
22	649	30.4	181	11	Q9D7R3	Q9D7R3 mus musculus
23	644.5	30.2	403	5	O61866	O61866 caenorhabdi
24	641.5	30.0	684	5	O95XV1	O95XV1 caenorhabdi
25	634	29.7	411	5	O20449	O20449 caenorhabdi
26	623.5	29.2	404	5	O16956	O16956 caenorhabdi
27	585.5	27.4	411	5	Q94252	Q94252 caenorhabdi
28	574.5	26.9	351	5	Q95X33	Q95X33 caenorhabdi
29	561.5	26.3	399	5	Q9VPE9	Q9VPE9 drosophila
30	548.5	25.7	434	5	Q9VKT9	Q9VKT9 drosophila
31	546.5	25.6	426	5	O17766	O17766 caenorhabdi
32	546	25.5	456	5	Q9VK55	Q9VK55 drosophila
33	542.5	25.4	398	5	Q9V796	Q9V796 drosophila
34	511.5	23.9	416	5	Q9VQ05	Q9VQ05 drosophila
35	511	23.9	616	5	O77107	O77107 plodia inte
36	508	23.8	457	5	Q9VKT2	Q9VKT2 drosophila
37	508	23.8	457	5	O8T3X7	O8T3X7 drosophila
38	502.5	23.5	559	5	O17219	O17219 bombyx mori
39	495	23.2	435	5	Q9VG46	Q9VG46 drosophila
40	482.5	22.6	838	5	Q9VVK6	Q9VVK6 drosophila
41	477	22.3	406	5	Q9VKT7	Q9VKT7 drosophila
42	469.5	22.0	401	5	O9U276	O9U276 caenorhabdi
43	445.5	20.8	457	5	O95U37	O95U37 drosophila
44	437	20.4	169	11	Q9D2L7	Q9D2L7 mus musculus
45	436	20.4	443	3	P78898	P78898 schizosacch

ALIGNMENTS

RESULT 1

ID	Q9D798	PRELIMINARY;	PRT;	395 AA.
AC	Q9D798;			
DC	01-JUN-2001 (TREMBlrel. 17, Created)			
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)			
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)			
DE	2310051B21RIK protein.			
GN	2310051B21RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=TONGUE;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,			
RA	Hayashizaki Y.;			
RT	*Functional annotation of a full-length mouse cDNA collection.*;			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK009431; BAB26283.1; -;			
DR	MGD; MGI:1914967; 2310051B21RIK.			


```
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44603 MW; 3DFDB86F6A671E3E CRC64;

Query Match 49.6%; Score 1059.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 3.1e-79;
Matches 196; Conservative 66; Mismatches 124; Indels 3; Gaps 2;

QY 2 MWLLTTTCLCGTUNAGFLDLENEVNPVWMTSEIIINGYSEYEVTTEDGYILL 61
DB 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNYSQMITWGYSEYEVTTEDGYILG 59

QY 62 VNRIPYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 60 VYRIPYGRKNSENICKRPVAYLOHGLIASATWNIINLNNLSLAFILADAGYDVWNGNSRG 119

QY 122 NTSRRHKTLSDEKFWAFSDEMAKYDLPGVIDFIVNKTQGEKLYFIGHSLGTTIGFV 181
DB 120 NTSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVOKTQGEKIHYVGHSGTTIGFI 179

QY 182 AFSTMPLEAQRKMFALPGPTISFKYPTGIFTRFELLNSIIKAVFGTKGFLEDKTKYI 241
DB 180 AFSTNPALAKKIKRYPALAPVATVYTESPKKISLIPKFLKVIFGNKMFPHNYLQDF 239

QY 242 ASTKCNKILWLCSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNILHIKOLYHS 301
DB 240 LGTEVCSRELLDLCSNALFICFGDKKNLNVSRDLVGHNPAGTSTQDLEFWHAQLAKS 299

QY 302 DEFRAIDMGNDADNNKHYNQSHPIYDLTAMKVPTAIWAGGHVILGTQPDVARILPQIKS 361
DB 300 GLQAYNNGSPLONNLHYNQKTPPYDVSAMTVPITAVWNGGHDILADQDVAMLLPKLPN 359

QY 362 LSLVLSLPEWEPTDFWGLDAPORMFS 390
DB 360 LLYHKELP--YNHLDFIWMADPOEVYN 386

RESULT 2
Q9D6T5
ID Q9D6T5 PRELIMINARY; PRT; 395 AA.
AC Q9D6T5;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310061A13, full insert sequence.
GN 2310051B2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Washima J., Mazzarelli J., Wombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sagaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL; AK010236; BAB26787.1; -
DR EMBL; AK009413; BAB26727.1; -
DR EMBL; AK009428; BAB26280.1; -
DR EMBL; AK009459; BAB26300.1; -
DR EMBL; AK009473; BAB26312.1; -
DR EMBL; AK009474; BAB26313.1; -
DR EMBL; AK009479; BAB26316.1; -
DR EMBL; AK009523; BAB26338.1; -
DR EMBL; AK009525; BAB26339.1; -
DR EMBL; AK009546; BAB26352.1; -
DR EMBL; AK009571; BAB26368.1; -
DR EMBL; AK009573; BAB26370.1; -
DR EMBL; AK009729; BAB26466.1; -
DR EMBL; AK009773; BAB26495.1; -
DR EMBL; AK010019; BAB26647.1; -
DR EMBL; AK010035; BAB26656.1; -
DR EMBL; AK010058; BAB26673.1; -
DR EMBL; AK010061; BAB26675.1; -
DR EMBL; AK010124; BAB26715.1; -
DR EMBL; AK010125; BAB26716.1; -
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estr_ site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44637 MW; D3F96B65EA671E34 CRC64;

Query Match 49.5%; Score 1057.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 4.5e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGLDLENEVPEVMMNTSEIIYNGVPSSEYEVTTEDGYLL 61
Db 1 MWLLLVTS-VLSAFGGAGHGLGKLPKNPEANMVSQMITWGYPSSEYEVTTEDGYLL 59

QY 62 VNRIPTYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
Db 60 VYRIPTYGKNSENIGKRPVAYLQHLGLASATNWTNLPNNLSAFILADAGYDVMGNSRG 119

QY 122 NTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYDLPATIDFIVKTGOEKIHYVGHSGQTTIGFI 179

QY 182 AFSTMPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKLVFGNKMFMHNYLDQF 239

QY 242 ASTKICNKLWLICSEFMSLWAGSNKKNQSRMDVYMSHAPGSSVHNLIHLKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALFIFCGFDKKNLNSREDYVYLGHNPAQTSTQDLFWHAQLAKS 299

QY 302 DEFAYDWGNDADNKNHYNQSHPIYDLTAMKVPTAIWAGHDVLTGPQDVARILPOLKS 361
Db 300 GKLAQYNGWSPQLNMLHYNQTPPYDYVSAMTVPVIAVNGGHDILADPDQVAMLLPKLPN 359

QY 362 LSLVLSLLPEWPTTFDFVWGLDAPQRMFS 390
Db 360 LLYHKELP--YNHLDFIWMADAPQEVYN 386

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RESULT 4

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Q9D6Q6
ID Q9D6Q6 PRELIMINARY; PRT; 395 AA.
AC Q9D6Q6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310067K20, full insert sequence.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010093; BAB26697.1; -
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000374; Lipase.
DR InterPro; IPR000379; Ser_estr_ site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44623 MW; 245055F5E7FF07C9 CRC64;

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Query Match 49.4%; Score 1056.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 5.5e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLICGTLNAGGLDLENEVPEVMMNTSEIIYNGVPSSEYEVTTEDGYLL 61
Db 1 MWLLLVTS-VLSAFGGAGHGLGKLPKNPEANMVSQMITWGYPSSEYEVTTEDGYLL 59

QY 62 VNRIPTYGRTHARSTGPRPVYMOHALFADNAYWLENYANGSLGFLADAGYDVMGNSRG 121
Db 60 VYRIPTYGKNSENIGKRPVAYLQHLGLVASATNWTNLPNNLSAFILADAGYDVMGNSRG 119

QY 122 NTWSRRHKTSETDEKFWAFSDEMAYDLPVDFIVNKTGOEKLFIHSLGTTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYDLPATIDFIVKTGOEKIHYVGHSGQTTIGFI 179

QY 182 AFSTMPELAQRKKNFALGPISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKLVFGNKMFMHNYLDQF 239

QY 242 ASTKICNKLWLICSEFMSLWAGSNKKNQSRMDVYMSHAPGSSVHNLIHLKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALFIFCGFDKKNLNSREDYVYLGHNPAQTSTQDLFWHAQLAKS 299

QY 302 DEFAYDWGNDADNKNHYNQSHPIYDLTAMKVPTAIWAGHDVLTGPQDVARILPOLKS 361
Db 300 GKLAQYNGWSPQLNMLHYNQTPPYDYVSAMTVPVIAVNGGHDILADPDQVAMLLPKLPN 359

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QY 362 LSLVLSLLPEWPTDFVWGLDAPQMFS 390
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AC Q9D6P3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310069p19, full insert sequence.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010139; BAB26725.1;
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44651 MW; E48A73CCCBFD359D CRC64;

Query Match 49.4%; Score 1056.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 5.5e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLGCTLNAGGFLDLENEVNPVMNTSEIIYNGVPSEYEVVTTEDGYILL 61
DB 1 MWLLLVTS-VLSAFGGANGLFGKLGPKNPEANMVNSQMITWGPSEYEVVTTEDGYILG 59
QY 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 60 VYRIPYKKNSENIGKRPVAYLQHGILASATNWTNLPNNSLAFILADAGYDVWLGNSRG 119
QY 122 NTSRRHKTLSLSTDEKFWAFSDFEMAKYDLPGVIDFVINKTGOEKLFIHSLGTTIGFV 181
DB 120 NTSRSKNYYSPDSVEFWAFSDFEMAKYDLPLATIDFVQKTGOEKIHYVGHSGSTTIGFI 179
QY 182 AFTWPELAQRKMNFAFGPTISFKYPTGIFTRFPLLSNIIKAVFGTKGFFLEDKTKI 241
DB 180 AFTWPAKAKIKRYALAPATVATKYTESPKKISLIPKFLKLVFGNKMFWPHNYLDQF 239

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DB 240 LGTEVCSRELLDLCSNALIFCFGDFKKNLVSRFDVYLGHNPAGTSTQDLFWHAQLAKS 299
QY 302 DEFRAIDMGNDADNMKHYNSHPPIYDLTAMKVPTAIWAGGHVLTGTPQDVARIILPQIKS 361
DB 300 GKLOAYNMGSPLOQNLHYNQKTPPYIDVSAMTVPYAVWNGGHDILADQDVAMLLPKLPN 359
QY 362 LSLVLSLLPEWPTDFVWGLDAPQMFS 390
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AC Q9D6X0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009875; BAB26556.1;
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44665 MW; 40CA6B67859A8C5B CRC64;

Query Match 49.4%; Score 1055.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 6.6e-79;
Matches 196; Conservative 65; Mismatches 125; Indels 3; Gaps 2;

QY 2 MWLLTTTCLGCTLNAGGFLDLENEVNPVMNTSEIIYNGVPSEYEVVTTEDGYILL 61
DB 1 MWLLLVTS-VLSAFGGANGLFGKLGPKNPEANMVNSQMITWGPSEYEVVTTEDGYILG 59
QY 62 VNRIPYGRTHARSTGPRPVVYMQHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
DB 60 VYRIPYKKNSENIGKRPVAYLQHGILASATNWTNLPNNSLAFILADAGYDVWLGNSRG 119
QY 122 NTSRRHKTLSLSTDEKFWAFSDFEMAKYDLPGVIDFVINKTGOEKLFIHSLGTTIGFV 181

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Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYKDYLPATIDFIVQKTQOEKIHYVHSGQGTIGFI 179
Qy 182 AFTSMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVGKGFLEDKTKKI 241
Db 180 AFTSNPALAKKIKRYALAPVATVKYTESPKKISLIPFKFLKVFIGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMOSRDVYMSHAPTSSVHNILHIKQLYHS 301
Db 240 LGTEVCSRELLDLCSNLFIFCGFDKKNLVSRFDVYLVGHNPAGTSTQDLFHWQAQAKS 299
Qy 302 DEFRAIDGNDADNMKNHYNQSHPPYDITAMKVPTAIWAGGHDVLGTPODVARILPQK 361
Db 300 GKQAYNMGSPQLNMLHYNQKTPPYDVSAMTPTPIAVWNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 360 LLYHKEILP--YNNHLDFTIWMADAPQEVYN 386

RESULT 7
Q9D6L9
ID Q9D6L9 PRELIMINARY; PRT; 395 AA.
AC Q9D6L9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310076L13, full insert sequence.
DE 2310051B21RIK.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Boffelli D., Bojunga N., Carninci P., Fujita M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010203; BAB26766.1; -
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00561; abhydrolase.1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44671 MW; E8936162510AA55C CRC64;

Query Match 49.4%; Score 1055.5; DB 11; Length 395;
Best Local Similarity 50.4%; Pred. No. 6.6e-79;
Matches 196; Conservative 64; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLNENVEVNMNTSEIIINYGPSEYEVTTDGYILL 61
Db 1 MWLLVTS-VLSAFGGAHGLGKLPKNPEANMNVSMQITYWGPSEYEVTTDGYILG 59

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Qy 62 VNRIPYGRTHARSTGPRPVYMQHALFADNAYWLENYANGSLGFLIADAGYDVMGNSRG 121
Db 60 VYRIPYGKKNSENIGKRPVAYLQGLIASATNWTNLPNSLAFILADAGYDVLGNSRG 119
Qy 122 NTWSRHRKTLSETDEKFWAFSDEMAYKDYLPATIDFIVQKTQOEKIHYVHSGQGTIGFI 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAYKDYLPATIDFIVQKTQOEKIHYVHSGQGTIGFI 179
Qy 182 AFTSMPELAQRKKNFALGPTISFKYPTGIFTRFFLLPNSIIKAVGKGFLEDKTKKI 241
Db 180 AFTSNPALAKKIKRYALAPVATVKYTESPKKISLIPFKFLKVFIGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMOSRDVYMSHAPTSSVHNILHIKQLYHS 301
Db 240 LGTEVCSRELLDLCSNLFIFCGFDKKNLVSRFDVYLVGHNPAGTSTQDLFHWQAQAKS 299
Qy 302 DEFRAIDGNDADNMKNHYNQSHPPYDITAMKVPTAIWAGGHDVLGTPODVARILPQK 361
Db 300 GKQAYNMGSPQLNMLHYNQKTPPYDVSAMTPTPIAVWNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLLPEWEPTDFVWGLDAPQRMES 390
Db 360 LLYHKEILP--YNNHLDFTIWMADAPQEVYN 386

RESULT 8
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ID Q9D7C5 PRELIMINARY; PRT; 395 AA.
AC Q9D7C5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Boffelli D., Bojunga N., Carninci P., Fujita M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009359; BAB26240.1; -
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase.1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44748 MW; 3BD43992458DE058 CRC64;

Query Match 49.3%; Score 1053.5; DB 11; Length 395;

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Best Local Similarity 50.1%; Pred. No. 9.7e-79;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

QY 2 MWLLTTTCICGTLNAGFLDLENEVPEVMWNTSEIIINGYSPSEEVVTEGGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKAPEANNNVSMQITWYGYSPSEEVVTEGGYILG 59
QY 62 VNRIPIYGRTHARSTGRPVVYVYMHAFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGRKNSENICKRPVAYLQHLGLIASAKNWIITLNPNSLAFILADAGYDVWNGNSRG 119
QY 122 NWTWSRRHKTLSSETDKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTFGV 181
Db 120 NWTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKTQOEKIHVYHSGQTTFGI 179
QY 182 AFSTWPELAORIKMNFALGPTISEKPYGTGIFTRFELLNPSIIKAVFGTKGFLEDDKTKI 241
Db 180 AFSTWPAKAKIKRYALAPVATVYTESPFKIIHIFKFLKLVIFGNKMFPHNYLDQF 239
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTECVSRELLDLCSNALFIFCGFDKKNLVSRFDVVLGHNPAGTSTQDLFHHWLAQLAKS 299
QY 302 DEFRAIDGNDADNNKHYNQSHPPYIDLTAMKYPTATWAGGHVDVLTGTPQDVARIILPQKS 361
Db 300 GKLOYNMGSPLONNMLHYNQKTPPYIDVSAMTVPYAVWNGGHDIADPDQVAMLLPKLPN 359
QY 362 LSLVLSLLEPEWTEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFTWMDAPQEVYN 386

RESULT 9
Q9D767 ID Q9D767 PRELIMINARY; PRT; 395 AA.
AC Q9D767; 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK009537; BAB26346.1; -
DR MGD; MGI:1914967; 2310051B21RIK.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.

DR InterPro; IPR000379; Ser_estr_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44607 MW; E43317C2254FA8EB CRC64;

Query Match 49.3%; Score 1052.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 1.2e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

QY 2 MWLLTTTCICGTLNAGFLDLENEVPEVMWNTSEIIINGYSPSEEVVTEGGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKAPEANNNVSMQITWYGYSPSEEVVTEGGYILG 59
QY 62 VNRIPIYGRTHARSTGRPVVYVYMHAFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGRKNSENICKRPVAYLQHLGLIASATNWIITLNPNSLAFILADAGYDVWNGNSRG 119
QY 122 NWTWSRRHKTLSSETDKFWAFSDEMAKYDLPVDFIVNKTQOEKLYFIGHSLGTTFGV 181
Db 120 NWTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKTQOEKIHVYHSGQTTFGI 179
QY 182 AFSTWPELAORIKMNFALGPTISEKPYGTGIFTRFELLNPSIIKAVFGTKGFLEDDKTKI 241
Db 180 AFSTWPAKAKIKRYALAPVATVYTESPFKIIHIFKFLKLVIFGNKMFPHNYLDQF 239
QY 242 ASTKICNNKILWLCSEFMSLWAGSNKNNQSRMDVYMSHAPTSSVHNILHIKOLYHS 301
Db 240 LGTECVSRELLDLCSNALFIFCGFDKKNLVSRFDVVLGHNPAGTSTQDLFHHWLAQLAKS 299
QY 302 DEFRAIDGNDADNNKHYNQSHPPYIDLTAMKYPTATWAGGHVDVLTGTPQDVARIILPQKS 361
Db 300 GKLOYNMGSPLONNMLHYNQKTPPYIDVSAMTVPYAVWNGGHDIADPDQVAMLLPKLPN 359
QY 362 LSLVLSLLEPEWTEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFTWMDAPQEVYN 386

RESULT 10
Q9C9P8 ID Q9C9P8 PRELIMINARY; PRT; 395 AA.
AC Q9C9P8; 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE 2310051B21RIK protein.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.,

Functional annotation of a full-length mouse cDNA collection.;

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RT Nature 409:685-690(2001).
RL EMBL; AK010116; BAB26711.1; -.
DR EMBL; AK009300; BAB26201.1; -.
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44579 MW; D22968665EA671D34 CRC64;

Query Match 49.2%; Score 1050.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 1.7e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVNPVWMTSEIIINYGYSEYEVVTEGDYIIL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPEANMNVSQMITYWGYSPSEYEVVTEGDYIIL 59
Qy 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGRKNSENIGKRPVAYLQHLIASATNWTNLPNNSLAFLADAGYDVWNGNSRG 119
Qy 122 NTSRRHKTLSDEKFWAFSDEMAYDLPQVIDFIVNKTQGEKLYFIHSLGTTIGFV 181
Db 120 NTSRKNNVYSPDSVEFWAFSDEMAYDLPATIDFIVQKTQGEKIHVYHSGQTTIGFI 179
Qy 182 AFSTPELAQRKKNFALGPISFYPTGIFTRFLLPNSIIKAVFGKGFLEDKKTKI 241
Db 180 AFSTPALAKKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNQSDVYHSHAPTGGSSVHNILHIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALIFCGFDKKNLNVSRGVYLGHPNAGTSDQDLFWHAQLAKS 299
Qy 302 DEFRAIDNGNDNMKNHYNQSHPIYDITAMKVPYTAIWAGGHDVLTGTPQDVARILPOIKS 361
Db 300 GRLQAYNGSLQNLMLHYNQKTPPYDVSAMTVPYAVNNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLPEWEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLDFTWAMDAPQEVYN 386

RESULT 11
Q9D760
ID Q9D760 PRELIMINARY; PRT; 395 AA.
AC Q9D760;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21Rik protein.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohtsuki S.,
RA Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
RL EMBL; AK009560; BAB26359.1; -.
DR MGD; MGI:1914967; 2310051B21Rik.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44885 MW; FE96B5EA670BEE CRC64;

Query Match 49.1%; Score 1049.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.1e-78;
Matches 195; Conservative 67; Mismatches 124; Indels 3; Gaps 3;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVNPVWMTSEIIINYGYSEYEVVTEGDYIIL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPEANMNVSQMITYWGYSPSEYEVVTEGDYIIL 59
Qy 62 VNRIPIYGRTHARSTGPRPVVYMOHALFADNAYWLENYANGSLGFLADAGYDVWNGNSRG 121
Db 60 VYRIPIYGRKNSENIGKRPVAYLQHLIASATNWTNLPNNSLAFLADAGYDVWNGNSRG 119
Qy 122 NTSRRHKTLSDEKFWAFSDEMAYDLPQVIDFIVNKTQGEKLYFIHSLGTTIGFV 181
Db 120 NTSRKNNVYSPDSVEFWAFSDEMAYDLPATIDFIVQKTQGEKIHVYHSGQTTIGFI 179
Qy 182 AFSTPELAQRKKNFALGPISFYPTGIFTRFLLPNSIIKAVFGTGFLEDKKTKI 241
Db 180 AFSTPALAKKIKREYALAPVATVRYTESPFKKISLIPKFLKLVIFGNKMFPHNYLDQF 239
Qy 242 ASTKICNNKILWLCSEFMSLWAGSNKKNQSDVYHSHAPTGGSSVHNILHIKOLYHS 301
Db 240 LGTEVCSRELLDLCSNALIFCGFDKKNLNVSRDVLGHNPAGTSDQDLFWHAQLAKS 299
Qy 302 DEFRAIDNGNDNMKNHYNQSHPIYDITAMKVPYTAIWAGGHDVLTGTPQDVARILPOIKS 361
Db 300 GRLQAYNGSLQNLMLHYNQKTPPYDVSAMTVPYAVNNGGHDILADPDQVAMLLPKLPN 359
Qy 362 LSLVLSLPEWEPTDFVWGLDAPORMFS 390
Db 360 LLYHKEILP--YNHLY-FIWAMDAPQEVYN 386

RESULT 12
Q9D766
ID Q9D766 PRELIMINARY; PRT; 395 AA.
AC Q9D766;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 2310051B21Rik protein.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009544; BAB26350.1; -.
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR SEQUENCE 395 AA; 44648 MW; CC69875653AA7A74 CRC64;

Query Match 49.1%; Score 1048.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.5e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCCLIGTLAGFLDENVPVNMNTSEIIYNGYPSEEVETEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPANNNVSMQITYMGYPSEEVETEDGYILG 59

Qy 62 VNRIPTYGTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLIADAGYDVWNGNSRG 121
Db 60 VYRIPTYGKNSENIGKRPVAYLHGLIASATNWTNLPNNSLAFILADAGYDVWNGNSRG 119

Qy 122 NTWSRRHKTLSDETKFWAFSDEMAKYDLPGVDFIVNKTQOEKLYFTGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKQTQOEKIHVYGHSGQTIGFI 179

Qy 182 AFSTWPELAQRKMNPFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYKTESPFKKISLIXFLKLVIFGNKMFMPYVLDQF 239

Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNHILHIKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLVSRDVLGHNPAGTSTQDLPHWAQLAKS 299

Qy 302 DEFAYDNGNDADNKHYNQSHPIYDLTAMKVPTAIWAGGHVILGTPODVARIILPQIKS 361
Db 300 GKLOAYNGWSPLQNLHYNQKTPPYVDVSAMTVPIAVWNGGHDILADPDVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWETPFDVWGLDAPQMFS 390
Db 360 LLYHKELP--YNHLDFIWMADPAQEVYN 386

RESULT 14
Q9D655 PRELIMINARY; PRT; 395 AA.
ID Q9D655
AC Q9D655;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310063K07, full insert sequence.
GN 2310051B21Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-C57BL/6J; TISSUE-TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK010026; BAB26651.1; -.
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR SEQUENCE 395 AA; 44650 MW; 03F16D53373A4D57 CRC64;

Query Match 49.1%; Score 1048.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 2.5e-78;
Matches 195; Conservative 65; Mismatches 126; Indels 3; Gaps 2;

Qy 2 MWLLTTTCCLIGTLAGFLDENVPVNMNTSEIIYNGYPSEEVETEDGYILL 61
Db 1 MWLLLVTS-VLSAFGAHGLFGKLGPKNPANNNVSMQITYMGYPSEEVETEDGYILG 59

Qy 62 VNRIPTYGTHARSTGRPVVYMQHALFADNAYWLENYANGSLGFLIADAGYDVWNGNSRG 121
Db 60 VYRIPTYGKNSENIGKRPVAYLHGLIASATNWTNLPNNSLAFILADAGYDVWNGNSRG 119

Qy 122 NTWSRRHKTLSDETKFWAFSDEMAKYDLPGVDFIVNKTQOEKLYFTGHSLGTIGFV 181
Db 120 NTWSRKNVYSPDSVEFWAFSDEMAKYDLPATIDFIVKQTQOEKIHVYGHSGQTIGFI 179

Qy 182 AFSTWPELAQRKMNPFALGPTISFYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFSTNPALAKKIKRYALAPVATVYKTESPFKKISLIXFLKLVIFGNKMFMPYVLDQF 239

Qy 242 ASTKICNNKILWLICSEFMSLWAGSNKKNMOSRMDVYMSHAPTSSVHNHILHIKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFICFGDKKNLVSRDVLGHNPAGTSTQDLPHWAQLAKS 299

Qy 302 DEFAYDNGNDADNKHYNQSHPIYDLTAMKVPTAIWAGGHVILGTPODVARIILPQIKS 361
Db 300 GKLOAYNGWSPLQNLHYNQKTPPYVDVSAMTVPIAVWNGGHDILADPDVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWETPFDVWGLDAPQMFS 390
Db 360 LLYHKELP--YNHLDFIWMADPAQEVYN 386

RESULT 14
Q9D796 PRELIMINARY; PRT; 395 AA.
ID Q9D796
AC Q9D796;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310051B21Rik protein.
GN 2310051B21Rik.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009437; BAB26287.1; -
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase.1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44684 MW; 9F6B6A85A81257F CRC64;

Query Match 49.0%; Score 1046.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 3.7e-78;
Matches 195; Conservative 64; Mismatches 127; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPEVMMTSEIIYNGYPSVEYVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITYWGYPSVEYVTTEDGYILG 59

Qy 62 VNRIPTYGTHARSTGPRPVYVMQHALFADNAYWLENYANGSLGFLLDAGYDVMGNRSRG 121
Db 60 VYRIPTYGKKNSENIGKRPVAYLQHLGLASATNWTINLPNNSLAFILADAGYDVMGNRSRG 119

Qy 122 NTSRRHRTLTSETDEKFWAFSFDMAKYDLPVDFIVNKTGQEKLYFIGHSLGTTIGFV 181
Db 120 NTSRKNVYSPDSVEFWAFSFDMAKYDLPATDFIVQKTGQEKIHYVGHSGQTTIGFI 179

Qy 182 AFTWPELAQRKKNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFTSNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKVFIGNKMFPHNYLDQF 239

Qy 242 ASTKICNKKILWLCSEFMSLWAGSNKKNMOSRMDVYMHAPTGSSVHNTHLKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFFCFGDKKNLNVSRFDVYXGHNPGACTSQDLFWHAQLAKS 299

Qy 302 DEFAYDWGNDADNKKHYNSHPPIYDLTAMKVPTAIWAGGHVDLGTPOQVARTILPOIKS 361
Db 300 GKLQAYNWGSPQLQNLHYNQKTPPYDVSAVTPIAVWNGGHDILADPDQVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390
Db 360 LLYHKEILP--YNHLDFIWAMDAPQEVYN 386

RESULT 15
Q9D6Q3 PRELIMINARY; PRT; 395 AA.
ID Q9D6Q3

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AC Q9D6Q3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310068C02, full insert sequence.
GN 2310051B21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK010103; BAB26703.1; -
DR MGD: MGI:1914967; 2310051B21Rik.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase.1.
DR PROSITE: PS00120; LIPASE_SER; 1.
SQ SEQUENCE 395 AA; 44638 MW; 4E52613BC98AB3F CRC64;

Query Match 48.9%; Score 1045.5; DB 11; Length 395;
Best Local Similarity 50.1%; Pred. No. 4.4e-78;
Matches 195; Conservative 63; Mismatches 128; Indels 3; Gaps 2;

Qy 2 MWLLTTTCLICGTLNAGGFLDLENEVPEVMMTSEIIYNGYPSVEYVTTEDGYILL 61
Db 1 MWLLLVTS-VLSAFGGAHGLFGKLGPKNPEANMNVSMQITYWGYPSVEYVTTEDGYILG 59

Qy 62 VNRIPTYGTHARSTGPRPVYVMQHALFADNAYWLENYANGSLGFLLDAGYDVMGNRSRG 121
Db 60 VYRIPTYGKKNSENIGKRPVAYLQHLGLASATNWTINLPNNSLAFILADAGYDVMGNRSRG 119

Qy 122 NTSRRHRTLTSETDEKFWAFSFDMAKYDLPVDFIVNKTGQEKLYFIGHSLGTTIGFV 181
Db 120 NTSRKNVYSPDSVEFWAFSFDMAKYDLPATDFIVQKTGQEKIHYVGHSGQTTIGFI 179

Qy 182 AFTWPELAQRKKNFALGPTISFKYPTGIFTRFLLPNSIIKAVFGTKGFFLEDKTKI 241
Db 180 AFTSNPALAKKIKRFYALAPVATVKYTESPKKISLIPKFLKVFIGNKMFPHNYLDQF 239

Qy 242 ASTKICNKKILWLCSEFMSLWAGSNKKNMOSRMDVYMHAPTGSSVHNTHLKQLYHS 301
Db 240 LGTEVCSRELLDLCSNALFFCFGDKKNLNVSRFDVYXGHNPGACTSQDLFWHAQLAKS 299

Qy 302 DEFAYDWGNDADNKKHYNSHPPIYDLTAMKVPTAIWAGGHVDLGTPOQVARTILPOIKS 361
Db 300 GKLQAYNWGSPQLQNLHYNQKTPPYDVSAVTPIAVWNGGHDILADPDQVAMLLPKLPN 359

Qy 362 LSLVLSLLPEWPTDFVWGLDAPQRMFS 390

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Db 360 LLYHKEILP--YNHLDFTWMDAQEVYN 386

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Job time : 97 secs